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**WO 02/059355 A2**

(54) Title: POLYNUCLEOTIDES FOR USE AS TAGS AND TAG COMPLEMENTS, MANUFACTURE AND USE THEREOF

(57) Abstract: A family of minimally cross-hybridizing nucleotide sequences, methods of use, etc. A specific family of 1168 24mers is described.

POLYNUCLEOTIDES FOR USE AS TAGS AND TAG COMPLEMENTS,  
MANUFACTURE AND USE THEREOF

FIELD OF THE INVENTION

5           This invention relates to families of oligonucleotide tags for use, for example, in sorting molecules. Members of a given family of tags can be distinguished one from the other by specific hybridization to their tag complements.

10       BACKGROUND OF THE INVENTION

          Specific hybridization of oligonucleotides and their analogs is a fundamental process that is employed in a wide variety of research, medical, and industrial applications, including the identification of disease-related polynucleotides in diagnostic assays, screening for clones of novel target  
15       polynucleotides, identification of specific polynucleotides in blots of mixtures of polynucleotides, therapeutic blocking of inappropriately expressed genes and DNA sequencing. Sequence specific hybridization is critical in the development of high throughput multiplexed nucleic acid assays. As formats for these assays expand to encompass larger amounts of sequence information  
20       acquired through projects such as the Human Genome project, the challenge of sequence specific hybridization with high fidelity is becoming increasingly difficult to achieve.

          In large part, the success of hybridization using oligonucleotides depends on minimizing the number of false positives and false negatives. Such  
25       problems have made the simultaneous use of multiple hybridization probes in a single experiment i.e. multiplexing, particularly in the analysis of multiple gene sequences on a gene microarray, very difficult. For example, in certain binding assays, a number of nucleic acid molecules are bound to a chip with the desire that a given "target" sequence will bind selectively to its  
30       complement attached to the chip. Approaches have been developed that involve the use of oligonucleotide tags attached to a solid support that can be used to specifically hybridize to the tag complements that are coupled to probe sequences. Chetverin et al. (WO 93/17126) uses sectioned, binary  
35       oligonucleotide arrays to sort and survey nucleic acids. These arrays have a constant nucleotide sequence attached to an adjacent variable nucleotide sequence, both bound to a solid support by a covalent linking moiety. These binary arrays have advantages compared with ordinary arrays in that they can be used to sort strands according to their terminal sequences so that each strand binds to a fixed location on an array. The design of the terminal  
40       sequences in this approach comprises the use of constant and variable

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sequences. United States Patent Nos. 6,103,463 and 6,322,971 issued to Chetverin et al. on August 15, 2000 and November 27, 2001, respectively.

This concept of using molecular tags to sort a mixture of molecules is analogous to molecular tags developed for bacterial and yeast genetics (Hensel et al., Science; 269, 400-403: 1995 and Schoemaker et al., Nature Genetics; 14, 450-456: 1996). Here, a method termed "signature tagged" mutagenesis in which each mutant is tagged with a different DNA sequence is used to recover mutant genes from a complex mixture of approximately 10,000 bacterial colonies. In the tagging approach of Barany et al. (WO 9731256), known as the "zip chip", a family of nucleic acid molecules, the "zip-code addresses", each different from each other, are set out on a grid. Target molecules are attached to oligonucleotide sequences complementary to the "zipcode addresses," referred to as "zipcodes," which are used to specifically hybridize to the address locations on the grid. While the selection of these families of polynucleotide sequences used as addresses is critical for correct performance of the assay, the performance has not been described.

Working in a highly parallel hybridization environment requiring specific hybridization imposes very rigorous selection criteria for the design of families of oligonucleotides that are to be used. The success of these approaches is dependent on the specific hybridization of a probe and its complement. Problems arise as the family of nucleic acid molecules cross-hybridize or hybridize incorrectly to the target sequences. While it is common to obtain incorrect hybridization resulting in false positives or an inability to form hybrids resulting in false negatives, the frequency of such results must be minimized. In order to achieve this goal certain thermodynamic properties of forming nucleic acid hybrids must be considered. The temperature at which oligonucleotides form duplexes with their complementary sequences known as the  $T_m$  (the temperature at which 50% of the nucleic acid duplex is dissociated) varies according to a number of sequence dependent properties including the hydrogen bonding energies of the canonical pairs A-T and G-C (reflected in GC or base composition), stacking free energy and, to a lesser extent, nearest neighbour interactions. These energies vary widely among oligonucleotides that are typically used in hybridization assays. For example, hybridization of two probe sequences composed of 24 nucleotides, one with a 40% GC content and the other with a 60% GC content, with its complementary target under standard conditions theoretically may have a 10°C difference in melting temperature (Mueller et al., Current Protocols in Mol. Biol.; 15, 5:1993). Problems in hybridization occur when the hybrids are allowed to form under hybridization conditions that include a single hybridization temperature that is not optimal for correct hybridization of all

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oligonucleotide sequences of a set. Mismatch hybridization of non-complementary probes can occur forming duplexes with measurable mismatch stability (Santalucia et al., Biochemistry; 38: 3468-77, 1999). Mismatching of duplexes in a particular set of oligonucleotides can occur under

5 hybridization conditions where the mismatch results in a decrease in duplex stability that results in a higher  $T_m$  than the least stable correct duplex of that particular set. For example, if hybridization is carried out under conditions that favor the AT-rich perfect match duplex sequence, the possibility exists for hybridizing a GC-rich duplex sequence that contains a

10 mismatched base having a melting temperature that is still above the correctly formed AT-rich duplex. Therefore, design of families of oligonucleotide sequences that can be used in multiplexed hybridization reactions must include consideration for the thermodynamic properties of oligonucleotides and duplex formation that will reduce or eliminate cross hybridization behavior within

15 the designed oligonucleotide set.

The development of such families of tags has been attempted over the years with varying degrees of success. There are a number of different approaches for selecting sequences for use in multiplexed hybridization assays. The selection of sequences that can be used as zipcodes or tags in an

20 addressable array has been described in the patent literature in an approach taken by Brenner and co-workers. United States Patent No. 5,654,413 describes a population of oligonucleotide tags (and corresponding tag complements) in which each oligonucleotide tag includes a plurality of subunits, each subunit consisting of an oligonucleotide having a length of from three to six

25 nucleotides and each subunit being selected from a minimally cross hybridizing set, wherein a subunit of the set would have at least two mismatches with any other sequence of the set. Table II of the Brenner patent specification describes exemplary groups of 4mer subunits that are minimally cross hybridizing according to the aforementioned criteria. In the approach taken

30 by Brenner, constructing non cross-hybridizing oligonucleotides, relies on the use of subunits that form a duplex having at least two mismatches with the complement of any other subunit of the same set. The ordering of subunits in the construction of oligonucleotide tags is not specifically defined.

Parameters used in the design of tags based on subunits are discussed in

35 Barany et al. (WO 9731256). For example, in the design of polynucleotide sequences that are for example 24 nucleotides in length (24mer) derived from a set of four possible tetramers in which each 24mer "address" differs from its nearest 24mer neighbour by 3 tetramers. They discuss further that, if each tetramer differs from each other by at least two nucleotides, then each 24mer

40 will differ from the next by at least six nucleotides. This is determined



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without consideration for insertions or deletions when forming the alignment between any two sequences of the set. In this way a unique "zip code" sequence is generated. The zip code is ligated to a label in a target dependent manner, resulting in a unique "zip code" which is then allowed to hybridize to its address on the chip. To minimize cross-hybridization of a "zip code" to other "addresses", the hybridization reaction is carried out at temperatures of 75-80°C. Due to the high temperature conditions for hybridization, 24mers that have partial homology hybridize to a lesser extent than sequences with perfect complementarity and represent 'dead zones'. This approach of implementing stringent hybridization conditions for example, involving high temperature hybridization, is also practiced by Brenner et. al.

The current state of technology for designing non-cross hybridizing tags based on subunits does not provide sufficient guidance to construct a family of relatively large numbers of sequences with practical value in assays that require stringent non-cross hybridizing behavior.

A multiplex sequencing method has been described in United States Patent No. 4,942,124, which issued to Church on July 17, 1990. The method requires at least two vectors which differ from each other at a tag sequence. It is stated that a tag sequence in one vector will not hybridize under stringent hybridization conditions to a tag sequence (i.e., complementary probes do not cross-hybridize) in another vector. Exemplary stringent hybridization conditions are given as 42°C in 500-1000 mM sodium phosphate buffer. A set of 42 20-mer tag sequences, all of which lack G residues, is given in Figure 3 of the specification. Details of how the sequences were obtained are not provided, although Church states that initially 92 were chosen on the basis of their having sufficient sequence diversity to insure uniqueness.

So while it is possible for a person knowledgeable in the field to design a small number of non-cross hybridizing tags, it is difficult to design a larger number such tags. A co-pending application of the owner of this patent application describes such a set of 210 non-cross hybridizing tags that have a practical value. A method described in international patent application No. PCT/CA 01/00141 published under WO 01/59151 on August 16, 2001. Little guidance is provided, however, for the provision of a larger set, say 1000 or so, of non-cross hybridizing tags. Since having sets of approximately 1000 non-cross hybridizing tags, or more, would be of considerable practical value, it would be useful to develop such a set.

Thus, while it is desirable with such arrays to have, at once, a large number of address molecules, the address molecules should each be highly selective for its own complement sequence. While such an array provides the

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advantage that the family of molecules making up the grid is entirely of design, and does not rely on sequences as they occur in nature, the provision of a family of molecules, which is sufficiently large and where each individual member is sufficiently selective for its complement over all the other zipcode molecules (i.e., where there is sufficiently low cross-hybridization, or cross-talk) continues to elude researchers.

#### SUMMARY OF INVENTION

A family of 1168 sequences was obtained using a computer algorithm to have desirable hybridization properties for use in nucleic acid detection assays. The sequence set of 1168 oligonucleotides was partially characterized in hybridization assays, demonstrating the ability of family members to correctly hybridize to their complementary sequences with minimal cross hybridization. These are the sequences having SEQ ID NOS:1 to 1168 of Table

I.

Variant families of sequences (seen as tags or tag complements) of a family of sequences taken from Table I are also part of the invention. For the purposes of discussion, a family or set of oligonucleotides will often be described as a family of tag complements, but it will be understood that such a set could just easily be a family of tags.

A family of complements is obtained from a set of oligonucleotides based on a family of oligonucleotides such as those of Table I. To simplify discussion, providing a family of complements based on the oligonucleotides of Table I will be described.

Firstly, the groups of sequences based on the oligonucleotides of Table I can be represented as shown in Table IA.

**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier	
1	1	1	2	2	3	2	3	1	1	1	3	1	2	2	3	2	2	3	2	3	2	1	1	
3	2	2	1	3	1	3	2	2	1	1	2	2	3	2	1	2	2	2	3	1	2	3	1	2
1	2	3	2	2	1	1	1	3	2	1	1	3	2	3	2	2	3	1	1	1	2	3	2	3
2	3	1	2	3	2	2	1	3	1	1	3	2	1	2	1	2	2	3	2	3	1	1	2	4
2	2	2	3	2	3	2	1	3	1	1	2	1	2	3	2	3	2	2	3	2	2	1	1	5
1	2	1	1	3	2	3	2	1	1	3	2	3	1	1	1	2	1	1	3	1	1	3	1	6
1	1	3	1	3	2	1	2	2	2	3	2	2	3	2	3	1	3	2	2	1	1	1	2	7
3	2	3	2	2	2	1	2	3	2	2	1	2	1	2	3	2	3	1	1	3	2	2	2	8
1	1	1	3	1	3	1	1	2	1	3	1	1	2	1	2	3	2	3	2	1	1	3	2	9
2	1	2	3	1	1	1	3	1	3	2	3	1	3	1	2	1	1	2	3	2	2	2	1	10
1	2	3	1	3	1	1	1	2	1	2	3	2	2	1	3	1	1	2	3	2	3	1	2	11
2	2	1	3	2	2	3	2	2	3	1	2	3	2	2	2	1	3	2	1	3	2	2	2	12
3	2	1	1	1	3	1	3	2	1	2	1	1	3	2	3	2	2	3	1	2	3	1	2	13
1	1	1	3	2	1	1	3	1	1	2	3	1	2	3	2	2	1	1	2	1	1	3	2	14
3	2	1	3	1	1	1	2	1	3	2	2	2	1	2	2	3	1	2	3	1	2	2	3	15
2	3	2	1	1	3	2	3	1	1	1	2	1	3	2	3	1	3	2	2	1	2	2	2	16

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
1 1 1 2 1 3 1 2 3 1 2 1 1 3 2 3 1 3 1 1 2 3	17
1 2 1 1 3 2 2 1 2 1 1 3 2 3 2 2 1 2 3 2 3 1 3 2	18
2 1 2 1 3 1 2 1 1 1 3 1 3 1 2 3 1 2 2 2 3 2 2 3	19
1 3 1 3 2 2 3 1 3 1 1 2 3 2 1 2 1 3 2 1 2 2 1 2	20
1 1 3 2 1 3 2 2 2 3 2 1 1 3 1 1 2 3 1 2 2 3 2 1	21
2 2 1 2 3 1 1 1 2 2 3 1 3 2 3 1 1 3 1 2 2 3 1 2	22
3 2 1 2 1 2 3 2 1 1 1 2 2 3 2 2 1 2 3 2 2 3 1 3	23
3 1 1 2 2 3 2 1 2 1 1 1 3 2 1 2 2 1 3 1 2 3 2 3	24
2 1 3 1 2 3 1 3 1 2 2 1 1 3 2 3 2 2 1 2 2 2 3 1	25
3 2 2 1 1 3 2 2 2 3 2 2 2 1 2 3 2 1 2 1 3 1 1 3	26
3 1 3 2 1 2 2 1 3 2 1 1 1 3 2 3 1 2 1 2 3 1 2 1	27
3 2 3 1 1 2 3 1 2 2 2 1 3 2 1 1 1 2 3 1 2 2 3 1	28
1 3 2 2 3 1 1 3 2 2 1 2 1 3 1 1 1 2 3 1 2 2 1 3	29
1 3 2 3 1 2 1 1 1 2 3 2 2 1 3 2 2 3 1 1 2 2 3 2	30
2 1 2 1 2 1 3 2 1 1 1 2 3 2 2 2 3 2 3 2 3 2 2 3	31
2 2 1 1 3 2 3 2 2 1 3 2 2 1 2 2 2 3 2 2 3 2 1 3	32
3 2 1 3 2 1 1 2 1 2 3 1 1 3 2 3 1 3 1 1 2 1 2 1	33
2 1 3 2 3 2 1 2 1 3 1 1 2 3 2 1 3 1 2 2 2 1 3 2	34
2 2 3 2 1 3 1 2 2 1 3 1 2 3 2 3 2 2 2 3 2 1 1 1	35
2 1 3 2 1 2 1 3 1 3 2 1 3 1 3 1 2 3 1 2 1 2 2 2	36
1 2 2 3 2 3 1 1 1 3 1 1 1 3 1 1 3 1 1 1 1 2 2	37
2 3 2 3 1 3 1 1 2 2 1 1 3 1 2 2 1 1 3 1 1 2 3 2	38
1 2 1 2 2 1 3 2 2 1 1 3 1 1 1 3 1 1 3 1 3 2 2 3	39
2 2 3 2 1 3 2 2 3 1 3 1 1 1 2 1 2 3 2 1 3 2 2 2	40
2 1 3 1 3 2 2 3 2 2 1 1 1 3 1 3 2 3 2 1 1 1 2 1	41
3 2 2 1 2 3 1 2 3 2 3 2 1 2 1 1 3 2 1 1 2 1 2 3	42
2 2 2 3 2 2 1 3 1 1 2 3 1 3 1 1 3 1 2 2 2 1 2 3	43
1 3 2 2 1 2 1 3 2 2 2 1 1 1 3 1 1 3 2 1 3 2 1 3 1	44
3 2 3 1 3 1 2 1 2 1 3 1 2 2 2 1 3 1 1 1 3 2 1 1	45
2 2 3 2 2 2 1 2 1 3 2 3 1 1 3 2 3 1 1 2 1 3 2 1	46
1 1 3 2 1 1 3 2 1 3 2 1 1 2 1 3 2 3 2 3 2 2 1 1	47
1 2 2 2 3 2 3 1 3 2 2 1 2 3 1 1 1 3 1 2 1 1 3 1	48
3 1 1 1 3 2 1 3 1 3 1 1 2 1 1 1 3 1 2 1 1 3 1 1	49
1 2 2 2 1 1 3 1 2 2 3 2 2 1 1 3 1 3 2 1 3 1 1 3	50
3 2 2 2 1 1 1 3 1 2 2 3 2 1 1 3 1 1 2 3 2 3 2 1	51
2 2 2 3 2 3 1 1 3 1 2 3 1 1 3 2 1 2 2 2 3 2 1 2	52
2 3 2 3 2 2 2 1 3 1 1 2 2 2 1 3 2 1 2 3 2 3 2 1	53
3 1 2 1 1 2 3 1 2 2 1 2 1 3 1 1 1 3 2 3 2 2 2 3	54
3 2 2 1 2 2 2 3 2 1 1 3 2 2 1 1 3 1 2 1 3 2 1 3	55
1 3 2 2 2 1 2 2 3 1 1 1 3 1 3 2 2 2 3 1 1 2 1 3	56
2 2 3 2 3 2 2 2 1 2 2 3 2 3 2 1 3 2 2 2 1 1 1 3	57
1 2 2 3 2 3 1 3 1 1 3 1 2 1 2 3 1 1 1 3 2 2 1 2	58
2 3 1 3 1 1 2 3 2 1 1 1 3 1 1 2 3 2 2 2 1 2 2 3	59
1 2 3 2 3 1 1 1 3 2 2 1 2 3 1 2 3 2 2 1 1 2 2 3	60
3 2 2 2 1 3 2 1 2 2 1 3 2 2 3 2 2 1 1 3 1 2 2 3	61
3 1 2 2 3 1 2 1 2 2 2 3 1 1 2 3 2 2 2 3 2 2 2 3	62
2 3 1 1 2 2 3 1 1 1 3 2 3 2 1 1 2 3 2 2 3 2 1 2	63
3 1 2 2 3 2 1 2 2 3 2 2 3 1 3 1 1 2 1 3 1 1 2 1	64
1 1 1 2 2 2 3 1 3 1 2 2 2 3 2 3 1 2 1 3 1 3 2 1	65
3 2 1 1 2 2 1 3 1 2 2 2 3 2 2 2 3 2 2 3 2 2 3 2	66
3 2 2 2 3 2 1 2 2 3 2 2 1 3 2 3 1 1 2 1 2 1 3 2	67
1 2 3 2 1 3 2 1 3 2 1 3 1 2 3 2 2 2 1 2 3 1 1 2	68
2 3 2 2 2 1 1 1 3 1 2 3 1 2 2 3 1 1 3 1 1 1 2 3	69
2 3 2 3 1 2 1 1 2 3 1 2 3 2 2 1 2 2 2 3 2 3 2 1	70
1 2 1 3 2 2 3 2 3 1 3 1 1 2 2 2 3 2 1 1 2 2 1 3	71
1 2 1 3 1 2 3 2 1 1 3 1 3 1 1 1 2 2 3 2 3 1 1 1	72

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Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
1 3 1 2 2 1 1 3 1 3 1 1 3 2 2 1 1 2 1 3 1 3 2 1	73
3 1 1 3 2 1 1 1 2 2 3 2 3 1 1 2 3 1 1 1 3 1 1 1	74
1 1 2 3 2 1 1 3 1 1 1 3 1 1 3 1 2 2 3 2 2 3 2 1	75
2 2 2 3 1 2 2 2 1 2 3 2 3 2 2 1 2 3 2 2 3 1 3 2	76
3 2 1 2 2 3 1 3 1 1 1 2 2 2 3 1 1 3 1 1 2 3 1 1	77
3 1 1 2 3 2 1 2 3 1 1 1 2 3 1 1 2 2 3 2 1 1 3	78
2 1 2 2 3 2 1 3 1 1 3 2 1 1 1 3 2 2 1 3 1 1 3 2	79
2 2 2 1 2 3 2 1 1 2 3 1 2 1 1 3 2 3 2 1 3 2 2 3	80
1 2 1 2 1 3 2 2 3 1 1 1 2 2 3 2 3 1 2 1 3 2 3 2	81
1 2 1 1 3 1 1 1 2 2 1 3 1 3 1 3 2 2 3 2 1 1 1 3	82
3 1 1 2 2 3 2 3 1 1 1 2 3 2 3 1 2 2 3 1 2 1 2 1	83
1 1 1 2 1 1 3 2 1 3 2 2 2 1 1 2 3 1 3 1 3 1 1 3	84
3 1 2 2 1 1 1 3 1 1 3 2 1 1 3 2 3 1 1 2 3 2 2 2	85
2 1 2 3 2 3 2 3 2 2 3 2 2 2 1 3 2 3 2 2 1 2 2 1	86
3 1 3 2 2 1 2 1 2 3 2 1 3 2 2 1 3 1 3 2 2 1 2 1	87
3 1 1 1 3 1 1 1 3 1 1 3 2 3 2 2 1 1 3 2 2 1 1 1	88
2 1 3 2 1 2 2 1 3 2 1 1 3 2 1 2 3 2 3 1 2 2 3 2	89
2 2 3 2 3 2 3 1 2 2 3 1 1 2 1 2 2 3 2 3 1 1 1 2	90
1 2 3 2 3 1 1 1 3 1 3 2 2 1 1 3 2 3 1 2 2 1 1 1	91
3 1 2 2 3 1 1 2 3 1 2 2 3 1 3 1 2 1 2 3 2 1 1 1	92
1 1 3 1 2 3 1 2 1 3 2 2 1 1 3 2 3 2 1 1 3 2 2 1	93
2 1 3 2 2 3 2 2 1 2 2 3 1 3 1 1 2 2 2 1 3 1 1 3	94
2 2 2 1 2 1 3 2 3 1 1 2 2 1 2 3 1 3 2 3 1 1 1 3	95
3 1 2 1 3 1 2 2 2 1 3 1 1 2 3 1 1 2 2 1 1 3 2 3	96
2 2 2 3 1 1 3 1 1 3 1 3 1 2 2 2 3 1 1 1 2 2 3 1	97
1 2 3 1 1 2 1 1 3 1 3 2 2 3 1 2 1 1 1 2 3 2 3 1	98
2 3 2 2 2 1 2 3 2 1 3 2 3 2 1 3 1 2 2 3 1 1 2 2	99
2 2 2 1 1 3 2 3 1 3 2 2 1 2 1 3 1 1 3 2 1 3 2 1	100
3 1 2 2 2 1 2 3 2 3 2 2 2 3 1 1 3 2 2 1 1 3 1 2	101
2 1 3 2 2 1 3 1 3 1 1 1 3 2 3 1 2 1 1 1 3 2 2 1	102
3 2 1 1 2 3 1 2 1 1 2 3 1 1 3 2 3 2 1 2 1 2 1 3	103
1 1 2 3 1 1 3 2 3 2 2 1 3 2 1 2 1 3 1 2 1 3 2 1	104
2 1 1 1 2 2 3 1 3 2 2 2 3 2 2 2 3 1 2 2 3 2 1 3	105
2 1 1 2 3 1 1 3 1 1 2 1 1 3 2 1 2 3 1 3 2 3 2 2	106
1 1 1 2 3 2 1 1 2 1 3 2 3 2 2 3 2 2 1 3 2 2 1 3	107
1 3 1 3 2 2 1 3 2 3 1 1 1 2 3 2 2 3 2 2 1 1 1 2	108
3 1 1 1 2 1 3 1 1 1 2 3 2 1 2 2 3 2 2 2 3 2 3 1	109
1 3 2 2 1 2 1 1 3 2 2 2 3 2 3 1 3 1 1 2 2 1 1 3	110
3 1 3 2 2 2 1 2 1 3 2 2 1 3 1 1 2 1 2 3 2 2 3 2	111
1 3 1 3 2 2 1 2 2 1 3 1 1 3 1 1 3 1 2 2 2 1 1 3	112
3 1 3 2 2 1 1 2 3 1 1 1 2 1 1 3 2 1 2 2 2 3 2 3	113
1 2 3 1 2 3 1 1 2 1 3 2 2 3 1 1 3 2 1 2 1 2 1 3	114
1 2 1 3 1 2 1 2 3 1 3 1 2 3 1 1 1 3 2 2 1 3 2 1	115
2 1 2 3 2 1 1 1 3 1 1 1 3 2 3 1 1 1 3 1 1 3 1 1	116
2 3 1 1 2 3 2 1 3 1 1 1 2 3 1 1 2 3 2 2 3 1 1 1	117
1 1 2 2 3 1 1 2 1 3 2 3 2 3 2 3 1 3 2 2 2 1 1 2	118
1 3 1 2 1 2 2 3 2 2 2 3 1 2 2 1 1 2 3 1 1 3 1 3	119
1 1 1 3 2 2 3 2 1 1 1 3 2 2 3 1 1 3 1 2 1 1 1 3	120
3 2 2 1 1 3 1 3 1 2 2 1 2 3 1 3 1 2 3 2 1 2 2 1	121
1 3 1 1 3 1 2 1 2 1 1 3 1 1 3 1 2 2 3 1 1 2 2 3	122
3 2 1 3 1 1 1 2 2 2 3 1 1 2 2 3 1 2 3 2 3 1 1 1	123
1 1 3 1 3 2 1 3 1 2 2 3 1 2 1 1 3 2 1 2 1 2 3 1	124
2 3 1 2 1 2 1 3 2 1 3 2 3 1 1 3 1 1 1 2 1 1 3 2	125
1 3 1 2 1 1 2 3 1 2 3 1 3 1 1 1 2 3 1 1 3 1 2 1	126
1 2 3 2 3 1 1 1 3 2 1 2 2 2 3 2 3 1 2 1 2 1 3 2	127
1 1 2 1 1 3 1 3 1 1 2 2 3 1 2 1 2 3 1 1 3 1 2 3	128

Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern																							Sequence Identifier		
2	1	1	3	2	3	2	1	2	2	2	1	3	2	1	3	1	1	2	3	1	1	3	2	129	
2	1	2	3	2	2	1	3	1	2	2	2	3	2	2	3	1	3	1	2	2	3	1	2	130	
1	3	2	2	2	3	2	1	2	3	1	1	3	1	3	1	2	1	3	2	1	2	2	2	131	
3	1	3	1	1	1	2	3	2	2	1	2	3	2	1	2	2	2	1	3	2	1	3	2	132	
2	1	2	3	2	3	1	3	1	1	2	3	2	3	2	2	2	3	1	2	2	2	1	1	133	
3	2	1	2	3	2	2	2	3	2	2	2	1	2	1	3	1	1	2	3	2	1	2	3	134	
3	1	3	2	1	2	1	2	1	3	1	1	3	1	1	1	3	1	1	1	2	2	2	3	135	
1	2	3	1	3	2	3	1	1	3	2	1	1	1	2	3	2	1	3	2	2	1	2	2	136	
2	2	1	1	3	1	1	3	2	3	1	3	2	2	1	2	2	3	2	3	1	2	1	2	137	
1	2	3	1	1	1	2	3	1	3	1	1	2	1	2	2	3	2	2	3	2	2	2	3	138	
3	1	2	2	1	1	2	3	1	2	2	1	2	3	2	3	1	1	2	2	3	1	2	3	139	
3	1	1	1	2	3	2	2	1	1	1	1	3	1	2	1	2	3	1	1	1	3	2	1	3	140
2	1	2	2	3	2	2	3	1	2	2	2	3	1	2	1	2	2	1	3	2	3	2	3	141	
2	2	2	1	2	3	2	2	2	3	2	3	2	1	2	3	2	1	1	3	2	1	3	2	142	
1	1	2	2	3	1	1	1	3	1	1	2	2	3	2	3	2	3	1	1	2	2	3	1	143	
2	3	1	3	2	2	2	3	1	1	2	2	2	3	2	2	2	3	1	3	2	1	1	2	144	
3	1	2	3	2	1	2	1	1	2	3	1	2	3	2	3	2	3	2	1	1	1	2	2	145	
1	2	3	2	3	1	3	1	3	1	1	3	1	1	2	2	2	3	2	2	2	1	2	2	146	
3	2	3	1	2	1	1	1	3	2	1	2	2	3	2	2	2	3	1	2	1	3	1	1	147	
3	1	1	3	2	1	3	1	1	2	1	3	1	1	1	3	2	2	1	1	2	1	3	1	148	
2	2	3	2	3	2	1	3	2	2	1	1	3	1	3	2	2	3	2	2	2	1	1	2	149	
2	1	3	2	1	3	2	1	1	3	2	2	3	2	2	1	3	1	1	2	1	3	2	2	150	
1	1	2	2	2	3	1	1	3	2	1	2	1	1	2	3	1	1	2	3	2	3	2	3	151	
2	1	3	1	1	1	2	2	3	2	1	3	2	1	2	2	2	3	1	3	1	3	1	1	152	
2	3	2	1	2	1	2	3	2	2	1	1	2	3	1	3	1	2	3	2	2	3	2	1	153	
2	1	2	2	2	3	1	2	1	1	3	1	3	1	1	2	3	1	1	3	1	1	3	2	154	
2	2	3	1	1	2	1	3	2	3	2	1	1	2	3	1	1	2	1	2	3	1	2	3	155	
3	2	1	3	2	2	2	3	2	3	1	1	2	1	3	1	1	2	2	1	3	2	2	2	156	
1	1	1	3	1	2	3	1	2	2	3	2	1	1	2	2	2	3	2	3	2	3	1	1	157	
3	1	1	3	1	2	2	3	2	2	3	1	3	2	2	1	1	2	1	3	1	2	1	1	158	
1	3	1	2	2	1	2	3	2	1	3	2	3	1	2	3	2	1	1	1	2	3	2	2	159	
3	1	1	2	2	2	1	3	1	2	3	2	1	3	1	2	1	2	3	1	1	2	3	2	160	
3	1	2	1	3	1	1	3	2	3	2	1	2	2	1	1	3	2	1	1	3	2	2	1	161	
2	1	2	3	1	1	2	2	1	2	3	1	3	1	1	3	1	1	2	1	3	1	3	2	162	
2	2	2	3	2	2	1	2	3	1	1	3	2	3	1	2	2	2	3	2	2	2	3	2	163	
3	2	1	1	1	3	1	2	2	3	2	3	2	2	1	2	1	2	3	1	1	1	2	3	164	
2	2	3	2	3	1	2	1	3	2	1	3	2	2	1	3	1	2	1	2	2	2	3	2	165	
3	1	1	2	2	1	1	3	1	2	1	1	1	3	1	1	3	1	3	1	1	3	2	1	166	
3	1	2	2	3	2	1	3	1	1	1	2	3	1	1	2	2	2	3	2	1	3	2	1	167	
1	1	1	2	1	1	3	1	3	1	3	1	3	1	1	2	3	1	2	2	2	1	3	2	168	
1	1	2	2	1	2	3	2	3	1	1	2	1	3	1	2	2	3	2	2	3	1	1	3	169	
2	2	1	1	3	1	2	2	2	1	2	3	2	3	1	2	1	3	2	1	3	1	3	2	170	
2	2	1	1	1	3	1	2	1	3	2	3	2	2	2	3	2	2	3	2	3	2	2	1	171	
2	1	2	2	3	1	2	2	2	1	2	3	1	1	3	1	3	2	1	2	1	3	2	3	172	
1	1	1	2	2	2	3	1	2	3	1	3	2	1	3	2	2	2	1	1	3	1	3	1	173	
1	2	1	1	1	3	2	2	3	2	2	2	3	1	2	3	2	2	2	3	1	1	2	3	174	
3	1	2	2	3	2	3	1	2	3	1	1	2	1	1	2	3	2	2	1	2	2	3	1	175	
3	1	2	3	1	1	3	1	1	1	2	1	2	3	1	2	1	2	3	1	1	2	1	3	176	
2	2	1	1	1	3	2	2	1	2	2	3	1	1	3	2	3	1	1	3	2	2	3	1	177	
2	2	3	2	1	1	3	1	1	1	2	1	3	1	3	1	2	2	2	3	2	3	2	2	178	
3	1	3	1	2	2	3	1	3	2	2	2	1	1	3	2	1	2	2	1	3	1	2	2	179	
1	3	2	3	1	2	1	1	2	1	2	1	3	1	1	2	3	1	2	1	1	1	2	3	180	
3	1	2	1	1	2	1	3	2	3	1	1	2	2	2	2	3	1	3	2	2	3	2	1	2	181
1	3	1	2	1	2	2	2	3	2	1	3	2	1	3	1	1	1	3	2	1	2	3	2	182	
3	2	2	1	2	3	1	1	2	3	2	2	3	1	1	2	2	2	3	1	1	2	3	2	183	
1	2	3	1	1	1	3	1	2	2	2	1	3	2	2	3	2	3	1	3	1	2	1	2	184	

**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier		
1	1	1	2	1	3	1	3	1	1	3	2	2	1	2	3	1	2	3	2	3	1	2	1	185	
2	2	1	3	2	3	1	3	1	1	1	2	3	2	2	2	1	1	2	3	2	3	1	2	186	
2	3	1	1	3	1	1	2	1	2	3	2	3	1	1	1	2	2	1	3	2	2	2	3	187	
3	2	2	2	3	1	2	1	3	2	2	2	1	1	2	3	1	3	2	1	2	2	3	1	188	
3	2	2	3	2	1	1	3	2	1	1	2	3	1	2	1	1	1	3	2	1	2	3	1	189	
2	1	1	3	1	3	2	1	3	2	1	1	2	2	3	2	2	3	2	2	2	1	3	1	190	
2	2	2	3	1	3	1	3	1	3	2	1	2	3	2	1	2	3	1	2	2	1	2	2	191	
1	2	2	3	1	2	2	3	2	3	1	1	2	2	1	3	1	2	1	3	1	1	3	1	192	
3	1	2	2	1	3	2	1	2	2	2	1	3	2	1	3	2	1	1	2	1	3	1	3	193	
2	1	2	3	2	1	2	2	1	3	1	3	1	2	1	2	2	3	1	1	1	3	2	3	194	
2	1	2	3	2	3	1	1	1	3	2	1	1	2	3	1	2	1	1	1	2	3	1	3	195	
3	2	1	1	2	2	1	3	2	1	1	2	3	1	2	2	2	3	1	1	2	3	1	3	196	
3	2	2	2	1	2	2	3	2	1	1	1	3	1	2	2	3	2	1	1	3	2	3	1	1	197
2	1	3	2	1	3	1	1	2	2	3	2	2	3	2	2	1	1	1	3	1	1	2	3	198	
2	1	2	2	3	2	2	1	3	2	2	1	2	3	2	1	3	2	3	2	3	2	1	1	199	
3	1	3	2	3	1	1	1	3	2	2	1	2	1	2	3	1	1	1	3	2	1	2	1	200	
1	2	1	2	1	3	1	1	3	2	2	3	1	2	3	1	3	2	2	2	1	2	3	1	201	
2	2	2	1	3	1	1	3	2	1	1	3	1	1	2	1	1	3	2	3	1	3	2	1	202	
2	3	2	3	2	1	2	1	1	3	1	2	1	2	2	2	3	2	1	1	3	1	1	3	203	
2	1	3	1	1	3	1	3	2	2	3	2	1	2	2	3	2	2	1	2	1	1	3	2	204	
3	2	3	2	2	1	2	2	1	3	2	2	2	1	1	3	2	2	1	3	1	3	2	1	205	
1	1	2	1	2	1	3	2	3	1	2	3	2	3	1	1	1	2	2	3	1	1	2	3	206	
2	2	1	3	1	3	1	1	2	1	3	1	3	2	3	1	2	2	1	2	1	3	2	2	207	
3	1	1	3	2	3	1	3	2	2	1	1	2	3	1	2	2	2	3	2	1	1	1	2	208	
1	1	2	3	2	1	1	1	3	2	1	1	1	3	1	1	1	3	2	3	1	2	3	1	209	
3	2	2	1	3	2	2	1	2	3	1	2	3	1	1	2	1	2	2	3	2	3	2	1	210	
1	1	1	2	3	1	3	2	2	1	3	1	3	2	1	3	1	1	2	2	1	2	3	2	211	
3	1	2	1	2	1	3	1	1	3	1	2	2	1	3	2	2	1	3	2	3	1	2	1	212	
1	2	1	3	2	2	2	3	2	2	3	1	3	1	2	2	2	1	2	3	1	3	2	1	213	
2	1	3	1	1	2	1	3	2	2	1	3	2	1	3	2	1	1	3	1	3	2	1	2	214	
3	1	1	2	2	2	3	2	1	2	2	3	2	3	1	1	3	2	2	2	1	3	2	1	215	
3	2	1	3	2	1	1	3	1	1	3	1	3	1	1	2	2	1	3	1	2	2	1	1	216	
1	1	2	3	2	3	2	2	1	2	3	2	1	2	3	2	1	1	1	2	1	3	2	3	217	
3	1	1	2	2	1	3	2	2	1	3	1	3	2	1	1	1	2	2	3	2	2	2	3	218	
3	1	1	1	2	2	3	1	1	3	1	2	1	3	2	1	1	3	1	1	1	2	3	1	219	
3	2	3	2	1	2	2	1	2	3	2	3	1	2	2	2	1	2	3	1	2	1	3	1	220	
2	1	2	2	1	2	3	1	3	1	1	1	3	2	2	3	1	1	2	1	3	2	1	3	221	
2	1	2	3	2	1	2	2	3	2	1	2	2	3	1	3	2	1	3	1	2	3	1	1	222	
3	2	3	1	2	2	3	1	1	2	1	3	2	1	3	1	2	2	3	2	2	2	1	1	223	
1	3	2	1	1	3	2	2	3	2	2	2	3	1	2	2	3	1	1	1	2	2	3	3	224	
3	1	1	3	2	2	2	3	1	2	2	2	1	1	3	2	2	2	1	1	3	1	1	3	225	
3	1	3	1	1	3	1	2	1	1	1	2	3	1	2	1	2	2	3	2	2	1	2	3	226	
1	2	3	1	2	3	1	3	2	2	3	2	2	1	1	2	1	3	2	2	1	3	2	2	227	
2	1	2	3	1	2	1	2	2	2	3	1	1	3	1	3	2	3	2	2	1	1	3	1	228	
3	1	3	1	2	3	1	2	2	1	1	1	3	2	3	1	2	2	2	1	2	3	1	1	229	
1	2	1	3	2	2	1	1	3	1	3	2	3	1	2	3	1	3	1	1	2	1	1	1	230	
2	2	2	1	2	2	3	2	2	1	3	1	2	1	1	1	3	1	3	2	2	3	1	3	231	
1	3	1	1	2	1	2	2	3	1	2	1	3	2	2	3	1	1	3	2	2	3	1	1	232	
2	1	3	2	3	2	1	1	1	3	2	3	2	1	3	1	2	2	3	2	1	1	1	2	233	
1	3	2	1	3	2	3	1	2	1	2	3	1	2	2	2	3	1	1	2	1	2	2	3	234	
2	3	2	1	2	2	3	1	1	2	2	1	3	1	1	2	1	3	2	3	1	3	1	1	235	
2	3	1	2	1	2	3	1	3	1	2	1	3	1	1	3	2	2	2	1	1	2	3	2	236	
3	1	1	3	1	1	3	2	1	1	3	2	1	2	1	1	1	3	2	1	1	1	2	3	237	
2	2	2	1	1	3	2	3	2	3	1	2	1	1	3	1	1	3	1	2	1	3	1	1	238	
2	1	2	2	3	2	2	3	1	1	2	3	2	3	2	2	2	1	1	1	3	1	3	1	239	
3	1	1	2	1	1	2	3	1	2	3	1	3	1	3	1	2	2	1	2	2	3	1	1	240	

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
2 1 3 1 3 1 1 1 3 1 3 1 3 1 1 2 2 3 2 1 2 2 1 1	241
1 2 3 2 1 2 1 1 2 3 1 3 1 2 1 2 3 2 2 3 2 3 1	242
1 1 2 1 3 1 2 1 1 3 1 2 2 3 1 2 2 3 2 3 2 2 3	243
2 2 2 3 1 2 3 1 2 1 1 2 1 3 1 1 3 1 3 1 1 2 3 1	244
1 3 1 2 3 1 1 2 1 1 3 2 2 3 2 3 1 1 2 3 2 2 2 1	245
1 3 1 2 3 1 1 1 3 1 1 1 3 2 3 2 1 3 1 1 2 1 2 2	246
2 3 2 2 1 1 1 2 3 2 1 2 3 2 1 3 2 1 1 2 2 3 1 3	247
2 1 3 2 1 3 2 3 2 3 1 1 3 2 2 1 2 2 2 3 2 2 1 2	248
1 3 2 3 1 1 2 3 2 2 2 3 2 1 1 1 3 1 3 2 2 2 1 1	249
3 1 2 1 1 1 2 3 1 3 1 1 2 2 3 1 3 2 1 1 2 2 3 2	250
2 3 1 2 3 1 3 1 1 1 2 2 3 2 2 2 1 1 3 2 3 2 2 2	251
1 1 1 2 1 1 3 2 1 3 2 3 2 3 1 3 2 1 1 2 1 3 2 1	252
2 1 2 3 1 1 1 2 1 2 3 2 3 1 2 1 3 2 1 1 3 1 3 1	253
1 2 2 3 2 1 1 3 1 3 2 3 1 2 2 1 2 1 3 1 2 3 1 2	254
1 3 1 3 2 1 1 3 1 1 2 3 1 1 1 3 1 3 1 2 1 1 2 1	255
2 1 1 3 2 1 1 3 2 1 3 1 2 3 2 2 1 1 1 3 1 3 1 2	256
1 1 1 2 1 3 1 1 1 3 1 1 2 2 3 2 1 3 1 3 2 1 3 2	257
1 2 1 3 1 2 2 2 1 1 3 2 3 1 1 3 1 3 1 3 2 2 1 2	258
3 1 1 2 3 2 2 2 3 2 1 1 1 2 3 2 1 2 1 3 1 2 1 3	259
1 1 1 2 1 3 1 1 2 3 1 3 2 1 3 2 3 1 1 1 2 1 2 3	260
2 2 3 1 1 2 2 1 2 3 2 1 3 1 3 1 1 1 3 2 1 1 1 3	261
2 1 3 2 1 1 1 2 2 3 1 3 1 3 2 1 3 2 2 3 1 1 2 2	262
2 3 2 1 1 1 3 2 3 2 2 2 1 2 1 3 2 3 2 3 2 1 1 2	263
1 2 1 2 3 1 2 2 2 3 1 3 1 2 3 1 3 1 1 2 3 2 1 1	264
1 1 2 1 2 2 3 1 2 1 2 3 2 3 2 2 3 2 3 1 1 3 2 1	265
1 3 2 3 1 3 1 2 2 1 2 3 1 3 2 1 2 2 3 1 2 2 2 1	266
2 2 3 2 1 2 2 2 1 3 1 2 1 3 2 3 1 3 1 2 2 1 2 3	267
1 2 1 3 1 1 1 2 3 1 1 1 3 1 2 1 3 1 2 1 3 1 1 3	268
3 1 2 2 3 2 1 2 1 2 3 2 1 1 1 3 2 1 3 2 2 2 1 3	269
2 1 2 3 1 1 2 3 2 2 1 2 2 3 2 3 2 3 2 2 3 1 2 2	270
3 1 2 1 2 2 1 3 2 1 3 1 3 2 1 1 3 2 1 2 1 2 2 3	271
2 3 1 3 1 2 3 1 1 2 2 2 3 2 3 2 2 1 2 3 1 2 1 2	272
2 1 2 3 1 1 2 3 1 1 3 2 1 1 1 3 1 3 1 2 3 2 1 1	273
3 1 3 2 3 1 1 2 2 2 3 2 2 3 2 1 1 2 2 3 2 2 2	274
1 3 1 1 1 2 2 3 2 1 3 1 3 2 2 1 1 2 2 3 2 3 2 1	275
3 2 3 2 2 1 1 2 3 1 1 1 3 2 2 3 2 3 1 1 2 1 1 2	276
2 3 2 3 1 2 2 2 3 2 2 1 1 3 1 1 3 1 2 2 1 1 2 3	277
1 3 2 1 3 2 1 2 2 3 2 1 1 1 3 2 1 2 1 1 1 3 1 3	278
2 3 1 2 2 3 2 2 3 2 1 2 1 3 2 2 1 2 2 3 2 3 2 1	279
3 1 2 2 3 2 1 3 2 2 2 1 1 2 3 2 2 1 1 3 1 1 2 3	280
1 2 3 1 1 1 2 1 1 3 1 1 1 2 2 3 1 3 2 1 3 1 3 1	281
2 1 2 3 1 2 3 1 2 1 2 2 2 3 2 2 3 2 1 2 3 2 3 2	282
2 2 2 1 3 1 3 2 2 2 3 1 2 2 1 3 2 1 2 3 2 2 2 3	283
1 1 2 1 1 3 1 3 1 2 2 3 2 3 1 2 3 1 3 1 1 1 2 1	284
1 1 2 3 1 1 2 1 3 1 1 2 1 3 1 3 1 1 2 3 2 1 3 1	285
3 2 1 3 2 1 3 2 1 1 2 2 2 3 1 1 2 3 2 2 2 3 1 1	286
1 3 2 3 1 3 2 1 1 2 2 3 1 2 2 3 1 2 2 3 2 2 1 1	287
3 1 1 2 1 1 2 3 2 2 2 1 3 2 3 2 3 2 2 3 1 1 1	288
1 2 1 2 3 1 1 1 3 2 1 3 1 3 1 1 1 3 2 3 2 2 1 2	289
2 3 1 3 2 2 1 2 2 3 2 1 2 2 2 1 3 2 2 2 3 1 1 3	290
2 1 3 2 2 3 1 3 2 2 2 1 1 1 3 2 2 3 1 1 1 3 1 1	291
2 1 1 1 3 1 3 2 3 1 2 3 2 1 1 1 2 1 3 1 1 3 2 2	292
2 3 2 1 3 2 3 2 2 2 1 3 1 3 2 1 1 3 2 2 1 2 2 1	293
1 3 1 3 1 2 2 1 1 2 3 2 3 2 2 3 1 1 1 3 1 2 2 1	294
3 2 1 1 2 1 1 3 2 2 3 2 3 1 1 1 3 1 1 3 1 2 2 1	295
3 1 3 1 2 3 2 2 1 2 1 3 1 2 1 1 2 3 1 1 1 3 1 1	296

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**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier		
2	2	2	1	3	2	2	3	1	2	2	3	2	2	3	1	1	2	1	3	1	3	2	1	297	
1	2	2	1	2	2	3	1	1	1	3	2	1	3	1	2	3	2	2	1	3	1	2	3	298	
2	2	2	1	2	3	2	3	2	3	1	2	2	3	1	3	2	3	2	2	2	1	1	2	299	
2	1	2	2	2	1	3	2	2	1	3	1	2	1	3	1	2	1	3	1	3	1	3	2	300	
1	2	3	2	3	2	2	2	1	2	3	2	3	1	1	1	3	1	2	2	2	3	2	1	301	
1	2	1	3	2	1	1	2	2	1	3	1	1	3	1	3	1	1	3	1	1	2	3	2	302	
2	1	2	3	1	3	2	3	1	2	2	1	3	1	1	2	2	3	2	1	2	2	2	3	303	
2	2	1	1	2	3	2	1	2	2	3	2	2	2	1	1	1	3	1	3	2	3	2	3	304	
1	2	1	3	1	3	1	1	2	2	1	1	3	1	1	2	2	3	2	2	2	3	1	3	305	
3	2	2	1	2	1	1	3	2	1	3	1	1	1	2	3	2	1	2	1	3	1	1	3	306	
1	3	2	1	1	2	2	1	3	2	2	2	3	1	1	1	2	3	2	3	2	1	3	2	307	
3	1	1	1	3	1	2	2	1	2	3	1	2	2	3	2	1	1	1	3	2	3	1	2	308	
3	2	1	1	3	1	2	2	1	3	1	1	3	2	2	1	1	2	3	1	1	3	1	1	309	
3	1	3	1	1	2	3	2	2	3	1	1	2	1	1	3	1	1	3	2	1	1	2	2	310	
2	2	1	1	3	1	3	2	3	2	2	2	3	1	1	2	1	3	2	3	2	2	2	1	311	
1	2	1	1	1	3	1	1	1	3	1	3	2	1	2	3	1	3	1	2	2	1	2	3	312	
1	3	2	2	1	2	2	3	1	2	2	3	1	1	3	1	2	3	1	3	1	1	1	2	313	
3	2	2	2	3	2	3	2	2	2	3	2	1	2	1	1	3	2	2	3	2	2	1	1	314	
2	2	3	2	1	2	3	2	2	3	1	3	2	2	2	1	3	1	2	2	1	1	2	3	315	
2	1	3	2	2	1	1	1	3	2	1	2	1	3	2	2	3	2	2	2	3	1	3	2	316	
1	1	1	2	2	2	3	2	3	2	2	2	3	1	3	1	2	2	2	3	2	1	2	1	3	317
2	1	2	2	1	3	2	3	2	2	1	2	3	1	2	1	1	1	3	1	3	1	1	3	318	
2	1	2	1	1	3	1	1	3	2	1	1	2	2	2	3	1	3	1	1	3	1	3	2	319	
2	1	1	3	2	2	3	1	3	1	2	3	2	2	2	3	2	2	2	3	1	2	1	1	320	
3	2	3	2	1	3	1	2	2	2	1	2	3	1	1	2	2	3	1	3	2	1	1	2	321	
2	1	2	1	3	1	3	1	1	3	2	3	2	2	2	1	3	2	2	3	2	1	2	1	322	
1	2	1	1	1	3	1	1	3	1	1	2	1	3	2	2	3	2	2	3	2	3	2	1	323	
1	3	1	2	2	3	1	1	1	2	1	3	1	2	2	1	3	1	1	1	3	2	2	3	324	
3	2	2	3	2	2	1	2	1	1	3	1	1	1	2	1	3	2	2	2	3	2	2	3	325	
1	3	1	1	1	2	1	3	1	3	2	1	1	3	1	3	2	3	2	2	2	1	1	1	326	
1	3	1	3	1	2	1	3	2	1	3	2	1	1	1	2	1	3	2	2	1	2	2	3	327	
1	1	1	2	3	1	2	2	3	2	3	2	1	1	3	2	2	1	2	3	2	1	2	3	328	
1	1	3	1	1	3	2	1	1	3	1	3	1	3	1	1	1	2	2	2	3	1	1	2	329	
3	2	3	2	3	2	1	2	2	2	1	3	2	2	3	1	2	1	1	2	2	3	1	2	330	
1	2	2	3	2	2	3	2	2	3	2	2	3	1	3	1	1	1	2	3	2	1	2	2	331	
1	3	1	2	1	1	3	2	2	1	1	1	3	2	1	1	1	3	1	3	1	1	2	3	332	
2	1	3	2	2	3	1	1	3	2	2	1	3	2	2	2	1	1	3	2	3	2	2	1	333	
1	3	2	1	1	3	1	1	2	3	2	1	1	2	1	2	3	1	2	3	1	2	1	3	334	
1	2	3	1	3	1	2	2	3	1	1	1	3	1	2	2	2	1	2	3	1	1	2	3	335	
2	3	1	2	2	3	1	1	2	2	1	3	1	3	1	3	1	1	2	3	2	1	2	1	336	
1	3	2	2	1	3	2	1	1	3	1	3	1	1	2	1	2	1	3	2	3	1	1	2	337	
1	2	2	1	1	3	1	2	2	3	2	1	2	1	3	2	2	1	3	2	3	1	2	3	338	
3	1	3	1	2	1	1	1	3	1	1	2	2	3	1	1	1	2	1	3	1	1	3	1	339	
1	3	1	3	2	1	1	1	2	3	2	2	1	1	3	1	1	1	3	1	1	3	2	2	340	
1	1	1	3	2	2	2	3	2	2	1	2	3	2	3	2	3	1	1	3	1	1	2	2	341	
1	2	2	3	2	3	2	2	2	1	1	3	1	1	1	2	1	2	3	1	2	3	1	3	342	
2	1	2	2	3	1	1	1	2	3	1	3	1	2	2	3	2	1	2	3	2	1	3	2	343	
1	2	2	2	3	2	3	2	3	1	2	3	2	2	2	3	1	1	1	2	1	2	3	1	344	
2	1	1	3	1	2	1	1	2	1	3	2	3	1	3	1	3	1	1	1	2	2	3	1	345	
1	2	2	2	1	2	3	1	2	2	1	3	2	3	2	1	1	3	2	3	2	2	3	2	346	
3	1	2	2	1	1	3	1	1	2	1	1	1	3	2	3	2	3	1	1	3	1	1	2	347	
3	2	1	1	2	2	3	1	2	3	1	1	3	1	3	2	2	1	3	2	2	2	1	2	348	
2	3	2	3	2	2	1	2	3	2	2	1	2	1	1	3	1	1	3	2	3	1	2	1	349	
1	3	1	3	1	1	1	2	2	3	1	1	2	2	2	1	3	1	1	1	2	3	2	3	350	
2	2	1	2	2	3	1	1	2	3	2	3	1	3	1	1	1	3	2	1	2	2	2	3	351	
2	3	2	2	1	1	2	3	1	3	1	1	3	1	2	1	1	2	3	1	2	1	3	2	352	



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Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
3 1 1 1 3 2 1 2 2 2 3 2 2 3 1 2 2 1 2 2 3 2 2 3	353
2 1 3 2 2 2 1 2 3 2 1 3 2 2 1 1 2 2 3 2 2 3 1 3	354
3 2 2 3 1 1 1 3 1 2 1 3 2 2 2 3 1 2 1 2 3 2 1 2	355
2 2 1 3 1 1 3 1 2 1 3 1 2 2 1 2 2 3 1 3 1 1 1 3	356
1 1 2 1 1 2 3 2 2 3 2 3 1 1 1 2 1 3 1 2 3 2 3 1	357
1 3 2 1 1 3 1 1 1 3 2 2 2 1 3 2 2 2 1 3 2 2 1 3	358
2 1 3 2 2 2 1 1 2 3 1 3 1 2 3 2 2 2 3 1 2 1 2 3	359
2 2 1 1 1 3 1 2 3 2 2 1 1 1 3 1 1 2 3 1 3 2 3 1	360
1 1 1 3 2 3 2 3 2 1 2 1 2 3 2 2 1 3 1 1 1 3 2 1	361
1 2 2 1 1 3 2 2 1 2 3 2 3 2 2 2 1 2 3 2 3 2 2 3	362
2 2 2 3 1 1 3 1 1 3 2 3 2 2 2 3 2 1 2 2 1 2 3 2	363
2 3 2 2 1 1 3 1 1 3 2 2 2 1 3 2 2 1 1 1 3 2 2 3	364
2 2 2 1 1 3 2 1 2 1 1 3 1 2 2 3 2 3 2 3 1 3 1 2	365
1 3 1 2 1 2 2 2 3 1 2 1 3 1 2 1 3 1 1 3 1 1 1 3	366
1 2 2 2 1 3 1 3 2 2 3 2 1 1 3 1 1 3 1 2 1 2 2 3	367
3 1 3 1 1 1 2 2 3 2 1 1 2 2 3 2 2 1 3 1 3 2 1 2	368
3 1 1 3 2 1 2 1 2 3 2 2 1 1 3 1 2 3 2 1 1 2 1 3	369
1 1 2 1 2 2 3 1 1 3 1 2 3 2 1 3 2 3 1 3 2 2 1 2	370
3 1 3 2 2 2 1 3 1 1 1 2 3 1 2 1 1 1 3 1 1 2 2 3	371
2 1 1 3 1 1 1 2 3 1 3 2 2 1 2 1 2 3 2 2 3 1 3 1	372
2 2 3 1 2 1 2 1 1 3 1 1 3 2 2 3 2 3 1 2 1 1 3 2	373
1 1 3 2 3 2 2 2 1 1 2 3 2 1 1 3 1 3 1 1 2 3 1 1	374
3 2 2 3 2 3 1 3 1 1 2 2 1 3 1 1 1 2 1 3 2 1 2 1	375
2 2 2 1 3 2 2 2 3 1 2 3 2 3 2 2 2 1 2 3 1 3 1 2	376
3 2 1 1 2 2 3 1 1 1 3 2 1 2 3 1 3 2 1 3 2 1 1 2	377
2 1 3 2 2 3 1 1 2 1 1 3 1 2 2 3 1 3 1 3 1 1 1 2	378
2 2 1 1 3 2 3 1 1 3 2 3 2 2 3 2 2 2 1 2 2 3 1 1	379
1 2 2 3 1 2 2 2 3 2 2 3 1 1 1 2 1 1 3 2 3 2 2 3	380
2 3 1 1 2 2 3 2 2 3 1 2 1 1 3 2 2 1 2 3 1 1 3 1	381
3 2 2 2 3 2 2 1 2 2 3 1 3 2 1 1 3 2 2 3 1 1 2 2	382
2 3 1 2 2 2 1 3 2 1 2 3 2 1 2 2 1 3 1 3 2 2 3 1	383
2 1 1 1 2 1 3 1 3 1 2 3 1 3 1 1 2 1 1 3 1 1 1 3	384
1 3 1 1 2 3 2 2 1 2 1 2 3 2 1 3 1 3 1 1 1 2 2 3	385
1 2 2 2 1 2 3 2 1 3 2 2 3 1 3 1 3 2 3 1 2 1 1 1	386
3 2 1 1 1 3 1 2 1 3 2 2 2 3 1 3 2 1 1 2 2 2 3 1	387
3 1 1 1 2 1 3 2 1 2 1 1 2 3 2 2 1 1 3 2 3 1 3 1	388
1 2 2 3 2 1 2 1 2 2 3 2 3 2 2 3 1 1 3 1 1 1 3 2	389
3 1 3 2 2 1 1 3 2 3 2 1 1 1 2 3 1 1 1 2 3 2 1 1	390
1 2 1 3 1 2 2 3 2 3 2 3 1 1 1 3 1 1 1 3 1 1 2 2	391
2 2 1 1 2 1 3 1 1 3 2 2 2 3 2 1 3 2 1 2 3 1 2 3	392
2 2 3 2 1 2 3 2 3 1 3 1 1 2 1 1 1 3 2 2 2 1 3 2	393
3 2 3 1 2 2 1 3 1 2 1 2 3 1 2 3 1 2 1 2 3 1 1 2	394
2 3 1 1 3 1 1 3 1 1 2 2 2 1 3 1 2 2 2 3 2 1 1 3	395
2 3 2 1 2 3 1 2 2 1 2 2 3 1 2 2 1 3 2 3 2 3 2 2	396
2 3 2 3 1 1 1 3 1 3 1 1 2 3 1 2 1 3 1 2 1 2 2 2	397
1 1 2 2 3 1 1 1 2 3 1 3 2 3 2 3 2 2 2 1 1 3 1 1	398
1 2 2 1 2 1 3 1 3 2 2 1 3 2 2 2 1 3 1 1 2 3 1 3	399
1 1 1 3 1 2 1 3 1 1 1 2 2 3 1 3 2 3 2 1 2 3 1 2	400
3 2 1 3 2 2 2 3 2 2 1 1 2 3 2 2 3 2 1 2 1 1 2 3	401
1 3 1 3 1 2 1 2 2 1 3 1 1 2 3 2 1 1 3 1 1 2 1 3	402
1 3 1 1 3 2 2 2 3 1 1 1 2 1 2 3 1 2 1 3 1 1 2 3	403
2 1 3 1 1 2 3 2 2 1 1 1 3 2 2 2 1 3 2 1 2 1 3 1 3	404
1 3 2 1 3 1 2 3 2 1 2 3 2 2 1 1 2 3 2 3 1 1 2 1	405
2 3 1 1 1 3 2 3 1 1 1 2 1 2 3 1 1 1 2 3 2 2 3 2	406
1 2 1 3 2 1 2 1 2 2 3 1 3 2 2 2 3 2 1 2 3 1 1 3	407
3 1 1 3 1 1 1 2 3 2 2 2 3 2 1 3 1 1 2 1 1 3 2 1	408

Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
1 1 2 3 1 3 2 1 2 2 3 1 1 3 1 1 1 2 3 2 1 2 1 3	409
3 2 3 1 2 1 3 1 1 2 2 2 3 2 3 2 2 2 1 1 2 3 1 1	410
2 3 2 1 3 2 1 2 3 1 1 3 1 1 2 1 1 2 3 1 1 1 2 3	411
1 2 1 3 1 1 3 2 2 1 1 2 3 1 2 1 1 2 2 3 2 3 2 3	412
3 2 3 1 2 2 3 2 1 1 3 2 1 1 3 2 1 1 1 3 1 2 1 1	413
2 1 2 3 2 1 3 2 2 2 3 2 3 2 2 1 2 2 2 3 1 1 3 1	414
2 3 1 3 2 1 1 3 2 2 2 3 2 1 2 3 2 2 2 1 1 3 2 1	415
2 1 1 1 2 3 2 1 2 3 1 3 2 3 2 3 2 1 1 1 3 1 1 1	416
3 2 1 1 3 1 3 2 1 2 2 3 1 1 1 2 2 1 3 2 1 1 3 1	417
3 2 2 3 1 3 2 3 2 1 1 1 3 1 2 2 1 2 2 3 1 2 1 1	418
1 3 2 1 2 3 1 3 2 2 1 2 2 1 3 1 2 1 1 1 3 2 3 1	419
1 2 2 2 3 2 2 1 2 1 3 1 3 2 2 3 2 3 2 2 3 2 1 2	420
2 1 1 2 2 1 3 2 1 3 2 3 2 3 2 2 3 1 1 1 2 2 2 3	421
2 3 2 1 2 2 3 1 3 1 2 2 3 2 2 1 2 2 3 2 1 2 2 3	422
3 2 2 1 2 2 1 3 1 1 3 1 3 1 2 1 1 2 2 3 1 3 2 2	423
2 2 3 1 3 2 2 3 2 3 1 2 2 1 1 3 2 1 3 2 1 2 1 2	424
3 1 2 1 3 2 1 2 1 1 2 3 1 2 2 3 1 1 3 2 1 1 2 3	425
3 2 3 1 1 1 3 1 2 1 2 2 2 3 1 3 1 3 1 2 1 1 1 2	426
1 3 2 2 1 2 3 1 2 2 2 3 1 1 3 1 1 1 2 2 3 2 2 3	427
3 2 1 1 3 2 1 2 2 2 3 1 1 2 2 2 3 1 2 3 1 3 2 2	428
2 1 1 2 1 3 2 3 2 2 1 2 1 1 3 2 3 1 1 1 3 1 3 2	429
1 1 1 2 3 1 1 2 2 3 1 2 3 2 3 2 1 2 1 2 3 1 1 3	430
1 3 1 1 1 3 2 3 1 3 2 2 3 2 2 1 1 3 2 1 2 2 2 1	431
2 2 2 1 2 3 2 3 2 3 1 1 2 2 3 2 3 2 1 2 1 2 1 3	432
3 2 1 1 2 1 2 3 1 2 1 3 1 1 1 2 3 2 1 1 1 3 1 3	433
3 1 3 1 1 2 2 3 2 2 2 1 1 1 3 1 2 1 3 2 2 3 2 1	434
3 1 1 2 2 2 3 2 2 1 1 3 1 1 2 3 1 3 2 2 2 3 1 2	435
1 2 1 3 2 3 1 2 3 1 2 2 1 1 1 3 1 3 1 1 2 2 2 3	436
1 2 1 3 1 2 3 2 2 2 1 3 2 2 3 1 3 1 2 2 1 2 2 3	437
1 1 3 1 3 2 3 2 1 1 1 2 1 3 1 1 1 3 2 3 1 2 1 2	438
2 3 2 3 2 1 2 2 3 1 2 2 3 2 2 3 1 3 1 2 1 1 1 2	439
2 1 3 2 1 2 1 3 2 3 1 3 1 1 1 3 1 3 2 2 1 1 1 2	440
1 1 1 3 1 2 1 1 3 1 1 1 3 1 3 1 2 3 1 2 3 2 2 2	441
3 1 1 3 2 2 1 2 2 3 1 1 1 2 1 3 1 3 1 1 3 2 1 2	442
1 2 3 2 1 2 3 2 1 2 1 3 1 1 1 3 1 3 2 1 1 1 2 3	443
3 1 2 3 2 2 2 3 2 1 1 1 3 1 2 2 3 1 1 1 2 2 3 1	444
1 1 2 2 2 1 3 1 3 1 3 2 1 2 2 2 3 2 3 2 2 3 2 1	445
1 1 2 2 2 3 2 2 2 3 1 1 1 3 1 1 1 3 2 1 1 3 2 3	446
1 1 1 3 1 3 2 1 3 2 3 2 2 1 2 2 3 2 2 1 3 1 2 1	447
3 2 1 2 3 2 2 3 2 1 2 1 2 3 2 2 3 2 2 3 1 2 1 2	448
3 2 1 3 1 1 2 2 2 3 2 2 3 1 3 2 1 2 2 2 3 2 1 1	449
1 2 3 1 1 2 2 2 1 3 2 2 1 3 2 3 2 1 1 3 1 1 1 3	450
1 2 3 1 2 1 1 3 1 1 1 2 3 2 2 3 1 2 3 1 1 3 2 1	451
2 2 3 1 2 3 1 2 3 1 1 3 1 2 1 1 2 3 2 1 3 1 2 1	452
1 3 1 2 3 1 2 1 2 3 1 2 1 2 1 3 1 2 2 1 3 1 2 3	453
2 2 3 1 1 1 3 2 2 1 3 1 1 1 3 1 2 1 3 1 2 3 2 2	454
3 2 2 2 1 1 2 3 2 2 1 3 2 2 1 3 1 1 1 3 2 1 1 3	455
3 1 3 1 2 2 2 1 1 3 2 2 2 3 1 1 3 2 3 1 1 1 2 1	456
2 2 2 3 2 2 1 3 2 1 3 2 2 3 2 2 1 2 1 1 3 1 3 1	457
2 1 2 3 1 3 1 1 2 1 3 2 2 2 3 2 2 1 3 2 3 1 1 2	458
2 2 3 1 1 1 3 2 2 2 1 1 3 1 1 3 1 3 1 2 1 1 3	459
1 1 3 2 3 1 3 2 2 3 1 1 1 2 3 1 1 1 2 1 2 3 2 2	460
3 2 2 1 3 1 1 1 2 3 1 1 1 2 3 1 3 2 1 3 2 2 1 2	461
2 1 1 3 2 1 2 2 3 2 1 2 2 2 3 2 3 2 3 2 3 2 1 2	462
2 3 2 1 2 2 1 3 2 1 1 1 3 1 1 3 1 3 1 3 1 1 2 1	463
3 1 3 1 1 3 1 3 1 1 1 2 1 1 3 2 2 3 1 1 1 2 1 1	464

Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
3 2 1 1 1 3 2 1 3 1 1 1 2 1 3 1 1 2 2 3 1 3 2 2	465
3 2 3 2 3 2 2 1 2 2 2 3 2 2 2 3 2 1 1 1 3 2 1 2	466
2 2 2 3 1 2 3 2 1 2 3 1 1 2 1 2 1 3 2 1 2 3 1 3	467
1 1 3 1 2 2 3 2 3 2 3 1 1 2 1 3 2 2 3 1 1 1 2 2	468
2 1 2 1 1 1 3 2 2 2 3 1 1 3 1 2 3 1 3 2 3 1 2 1	469
1 3 1 2 1 1 1 3 1 3 1 2 2 2 1 1 3 1 2 3 2 1 2 3	470
3 1 1 3 1 1 2 2 1 1 3 2 2 3 1 3 1 1 2 2 1 1 3 1	471
2 1 3 1 3 1 1 1 2 2 2 3 1 2 1 1 1 3 1 1 1 3 1 3	472
1 1 1 3 2 2 2 1 2 3 1 1 3 2 2 1 2 2 3 1 3 2 1 3	473
1 1 1 2 1 3 2 3 2 1 1 3 2 1 1 1 3 1 3 1 2 3 1 2	474
2 1 2 3 1 2 3 1 2 2 2 1 3 2 2 1 2 1 1 3 1 3 2 3	475
2 1 3 1 2 1 1 1 2 3 2 2 1 2 3 1 2 3 1 3 2 1 1 3	476
1 3 1 2 2 3 1 2 2 3 2 3 1 2 3 1 2 2 2 3 2 1 2 1	477
2 2 1 1 3 1 1 3 1 1 2 2 3 2 1 2 1 2 3 1 3 1 3 2	478
3 2 1 3 1 1 2 3 2 2 2 1 3 1 3 2 2 3 1 1 2 1 2 1	479
3 1 3 1 1 1 2 1 3 2 1 1 3 1 1 3 2 1 1 1 2 1 3 1	480
1 2 2 3 1 1 3 2 2 3 2 2 1 2 3 2 3 1 1 3 1 2 2 2	481
2 1 1 1 2 3 2 2 3 2 3 2 1 3 1 3 2 1 1 2 2 1 3 1	482
1 1 1 2 1 1 3 1 3 2 2 2 3 1 3 1 1 3 2 2 3 2 2 2	483
1 3 2 2 3 2 1 1 2 1 1 3 1 1 3 2 3 1 2 2 2 1 1 3	484
3 2 2 1 3 1 1 2 3 2 1 2 1 2 1 3 1 3 2 2 1 3 1 2	485
2 2 3 1 2 1 2 2 3 1 1 1 3 1 3 1 1 1 3 2 2 1 2 3	486
2 2 1 1 1 3 1 3 1 3 1 1 1 2 3 2 2 2 3 1 2 2 1 3	487
2 3 2 3 1 1 2 2 2 3 1 3 2 1 2 2 1 3 2 1 1 3 1 1	488
2 1 1 2 2 2 3 1 1 2 3 2 3 1 1 1 3 2 2 3 2 2 1 3	489
1 2 3 2 3 2 2 2 3 1 1 1 3 1 2 3 1 2 3 1 2 2 2 1	490
1 1 3 2 2 1 2 3 2 2 3 1 2 1 2 2 3 1 3 2 3 1 1 1	491
2 1 3 1 2 1 1 1 3 1 1 3 1 1 2 1 3 1 3 1 2 2 2 1 3	492
3 1 2 3 1 1 2 3 2 1 3 1 2 1 2 1 2 3 2 1 1 2 3 1	493
3 1 1 3 1 1 2 1 3 2 2 2 1 2 3 2 1 1 1 2 3 1 2 3	494
3 2 1 3 2 1 2 1 2 1 3 2 2 1 1 1 3 1 2 3 1 3 2 2	495
3 2 2 1 2 2 2 3 2 3 2 1 2 3 1 2 2 1 2 3 1 2 2 3	496
1 3 1 3 1 2 2 1 3 1 1 1 2 2 3 1 3 1 3 1 1 2 2 1	497
3 2 1 2 3 1 2 1 3 1 3 2 2 2 1 2 1 3 2 3 1 2 1 1	498
3 2 2 1 3 1 1 1 3 1 1 2 3 1 1 1 2 2 3 1 1 3 2 1	499
1 1 3 1 1 2 3 1 3 1 1 2 1 2 1 3 1 3 1 2 3 1 1 2	500
1 1 1 3 1 3 1 1 2 1 3 2 3 2 2 2 1 1 3 1 1 3 1 2	501
3 1 2 3 2 3 2 2 1 2 2 3 1 2 1 3 1 1 1 2 2 1 3 1	502
2 1 3 1 3 2 2 1 2 1 3 1 3 1 2 1 2 2 3 2 1 2 3 1	503
3 1 3 1 3 2 2 3 1 1 2 1 1 3 2 2 1 1 1 3 1 2 1 2	504
1 3 1 2 1 2 3 1 1 1 2 1 3 1 2 2 3 2 2 1 3 1 3 1	505
3 1 3 2 3 1 1 2 1 3 1 1 1 3 1 2 1 2 3 2 2 1 1 2	506
1 1 1 3 1 3 1 2 1 2 2 3 1 1 3 1 3 1 1 2 1 1 1 3	507
3 2 2 1 2 1 3 1 1 2 1 1 3 2 2 3 2 1 1 1 3 2 3 2	508
2 3 1 2 1 3 2 1 2 3 1 2 1 1 2 3 2 3 2 2 2 1 2 3	509
2 2 2 3 2 2 3 2 2 1 1 3 2 1 2 3 2 3 1 2 2 2 1 3	510
2 1 1 1 3 2 3 2 2 3 2 3 2 2 1 1 1 3 1 2 2 1 1 3	511
2 3 2 3 2 2 2 3 1 2 2 3 1 2 2 1 1 2 3 2 2 1 2 3	512
1 2 2 1 1 2 3 1 1 2 3 1 3 2 3 2 2 3 2 1 1 2 3 2	513
2 1 3 1 2 3 2 2 2 3 2 3 1 3 2 2 2 3 1 2 1 2 2 1	514
3 1 1 2 3 1 1 2 1 3 2 1 1 2 1 3 1 2 3 1 2 2 2 3	515
1 1 2 1 3 2 3 2 3 2 2 3 2 2 1 2 1 2 3 1 2 2 1 3	516
2 1 3 1 2 2 1 3 1 1 3 1 2 3 2 2 3 2 3 2 1 2 2 1	517
1 1 2 3 2 3 2 3 2 3 2 2 1 1 1 2 3 1 1 2 2 2 3 2	518
3 1 1 2 2 1 1 3 2 1 2 1 2 3 1 3 2 3 2 1 3 1 1 1	519
2 2 1 2 2 3 2 3 2 3 2 1 1 3 2 1 3 2 3 2 1 1 1 2	520

**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier	
3	2	1	3	2	1	1	1	3	1	3	1	1	2	2	3	2	2	2	1	3	2	1	2	521
1	1	3	2	2	2	3	2	1	1	3	1	1	3	2	1	3	2	2	3	1	1	2	1	522
1	3	2	2	1	2	1	3	2	1	2	1	3	2	1	3	2	1	2	1	3	1	3	1	523
3	1	1	1	3	1	1	1	2	3	2	3	2	1	2	1	3	2	2	2	1	1	2	3	524
2	2	3	2	3	1	3	2	1	1	2	3	1	1	2	3	1	2	3	2	2	1	2	2	525
3	2	1	3	1	3	2	2	3	2	1	1	1	2	1	3	1	3	1	1	2	1	1	1	526
1	2	2	1	1	2	3	2	1	3	1	2	2	3	2	1	1	3	1	3	1	2	1	3	527
2	2	1	3	2	3	2	3	2	2	2	3	2	1	3	1	2	1	3	1	1	2	2	1	528
1	3	1	3	1	3	2	2	2	3	2	3	2	1	2	1	2	3	2	1	2	1	1	1	529
2	2	1	1	3	2	2	2	1	3	2	3	1	3	1	2	2	2	3	2	2	1	1	3	530
1	2	3	1	1	3	2	2	2	1	2	2	3	1	1	2	1	3	2	1	3	2	3	1	531
1	2	1	2	2	2	3	2	3	2	2	3	2	1	2	3	2	2	2	3	2	3	1	1	532
1	1	1	3	2	3	2	2	2	1	2	1	3	1	1	3	1	2	2	2	3	1	2	3	533
1	1	3	1	3	1	2	1	2	3	1	2	2	2	3	2	2	1	3	2	2	3	2	1	534
1	1	3	1	1	3	1	1	1	2	3	1	3	2	3	1	2	1	1	2	3	2	1	1	535
2	1	3	2	3	2	2	2	3	1	2	1	2	3	2	2	1	1	3	1	1	3	2	2	536
3	2	1	3	1	1	1	3	2	3	1	2	1	3	1	2	2	1	3	2	1	1	2	1	537
3	1	2	1	1	1	2	3	2	2	1	1	3	2	2	1	3	2	1	2	3	1	2	3	538
1	3	1	2	2	1	3	1	1	3	1	1	2	2	3	2	2	2	1	3	1	1	2	3	539
1	2	1	2	2	2	3	1	3	1	1	3	2	3	2	3	1	1	1	2	3	1	1	2	540
2	3	1	3	2	1	1	1	2	1	3	2	2	2	1	2	3	1	3	2	1	3	2	1	541
2	2	1	3	1	3	1	3	2	1	3	1	2	1	1	1	3	1	2	2	2	3	1	2	542
1	2	2	3	2	2	2	1	1	3	2	2	3	2	2	3	1	2	1	1	3	1	2	3	543
3	2	2	3	2	1	1	1	3	2	2	1	1	1	3	2	3	2	3	1	1	2	2	2	544
1	2	1	3	1	2	2	3	2	3	2	3	2	2	2	3	2	2	1	2	1	3	2	1	545
3	2	1	1	3	2	2	1	2	2	3	1	1	2	3	1	1	2	3	1	2	1	2	1	546
2	1	3	1	2	2	1	3	2	2	3	1	2	1	1	3	2	3	2	3	2	1	1	2	547
1	1	1	2	3	2	1	1	1	2	3	1	1	3	1	3	2	3	2	2	2	3	2	2	548
3	1	2	1	3	1	1	3	1	1	1	2	3	2	1	2	1	2	1	3	2	3	1	2	549
2	1	2	1	3	1	3	2	3	2	1	2	3	2	2	1	2	3	1	2	1	1	1	3	550
2	1	2	3	1	1	3	2	3	1	2	1	1	3	1	2	3	1	1	3	1	1	2	2	551
2	3	2	2	3	1	3	1	1	2	1	3	2	1	1	3	1	3	1	1	2	2	2	1	552
2	1	3	1	2	1	1	2	3	2	3	1	1	3	2	1	1	2	1	1	3	2	3	1	553
3	2	1	2	2	1	2	3	1	2	3	1	2	1	3	2	1	3	2	1	1	3	2	1	554
1	3	1	2	1	2	3	1	2	2	2	1	3	2	1	2	2	3	1	1	2	3	2	3	555
1	1	2	2	1	1	3	2	2	2	3	2	1	3	1	3	2	3	1	2	2	2	3	1	556
1	1	3	1	1	1	2	1	3	1	2	3	2	1	3	2	1	1	3	1	2	3	2	2	557
2	2	3	1	3	1	1	3	2	2	3	2	2	3	2	1	1	2	1	1	3	1	1	2	558
1	3	2	3	2	3	1	1	1	2	1	3	2	3	1	1	1	3	2	2	2	1	1	1	559
2	2	2	1	2	3	2	1	3	2	1	3	1	2	2	2	1	2	3	2	3	1	1	3	560
1	2	2	1	1	2	3	1	3	1	1	1	2	2	1	3	2	3	2	3	2	2	1	3	561
1	2	3	2	2	1	1	2	1	3	2	3	1	2	1	3	2	1	1	1	3	2	3	1	562
2	1	2	3	2	2	3	1	2	1	1	1	2	3	1	2	2	1	2	3	1	3	2	3	563
2	2	1	2	2	1	3	1	3	2	2	3	2	3	2	3	2	3	1	2	1	2	1	2	564
2	3	2	2	3	2	2	1	2	3	1	2	2	3	1	3	2	2	1	3	1	1	2	1	565
1	1	2	2	2	3	1	3	2	2	1	1	3	1	1	3	1	1	3	2	3	2	1	1	566
1	1	1	3	1	2	1	1	1	3	2	2	1	1	3	2	3	2	2	3	2	1	3	567	
2	3	2	2	3	1	3	1	2	3	1	2	1	2	2	3	2	1	2	1	1	3	2	2	568
2	1	1	1	2	1	3	2	3	1	1	2	3	1	3	2	2	1	2	1	3	1	3	2	569
1	2	1	3	1	2	3	2	2	1	2	3	1	2	1	3	2	2	1	3	2	2	1	3	570
3	2	2	1	1	3	2	3	1	1	3	1	2	1	2	3	2	1	2	2	3	2	2	1	571
2	1	1	3	1	1	1	3	2	1	1	1	3	2	2	2	3	2	1	3	1	2	3	2	572
1	1	3	1	3	1	1	1	3	2	2	2	3	1	2	2	3	1	1	2	1	1	1	3	573
1	2	1	2	2	1	3	1	2	3	2	3	1	3	2	2	1	2	1	2	3	2	3	2	574
1	3	2	2	2	3	1	3	2	2	2	1	3	2	1	2	2	3	2	3	1	1	2	1	575
1	2	3	2	2	1	1	1	2	3	1	3	1	3	1	2	2	3	2	3	2	1	2	1	576

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
2 1 1 1 2 3 2 2 3 2 3 1 2 2 1 2 2 3 2 3 1 3 1 2	577
2 1 1 3 1 1 2 2 3 1 1 3 2 1 1 3 1 3 2 2 1 2 2 3	578
1 3 1 3 1 2 1 3 1 1 2 2 1 1 3 2 2 2 3 2 2 3 1 2	579
3 1 1 3 1 1 2 3 2 2 1 1 3 1 1 1 2 1 2 3 2 1 1 3	580
2 1 2 2 2 3 2 3 1 2 2 1 1 3 1 1 3 2 2 3 1 3 1 1	581
1 3 2 2 1 3 1 1 2 2 2 3 2 3 2 1 3 2 1 3 1 1 2 2	582
1 1 3 2 2 2 1 2 2 3 2 2 3 1 2 3 2 2 3 2 1 2 2 3	583
3 1 1 2 3 1 3 2 2 2 1 1 3 1 3 2 2 2 1 2 1 3 2 1	584
1 3 2 3 1 1 3 1 2 2 3 2 1 2 3 2 1 3 2 1 2 1 1 1	585
1 3 2 2 3 1 1 1 2 3 1 3 2 1 2 2 1 1 3 2 1 1 2 3	586
1 2 3 2 3 2 2 1 2 2 2 3 1 3 1 2 3 1 3 2 1 1 2 2	587
1 1 1 2 1 3 2 3 2 2 3 2 2 3 1 1 3 2 2 3 2 2 1 2	588
3 2 1 3 1 3 1 1 1 3 1 2 1 2 1 2 3 2 1 3 2 2 2 1	589
3 1 3 1 3 2 1 2 2 2 3 1 2 3 1 1 2 3 1 2 2 1 2 1	590
3 1 3 2 1 2 1 1 3 2 2 2 1 3 2 3 2 1 2 1 2 2 3 1	591
1 2 1 1 2 3 2 3 1 2 2 1 2 2 3 1 2 2 3 1 3 1 3 1	592
2 2 1 3 2 2 3 2 2 1 2 3 2 3 1 3 1 3 2 1 1 2 1 1	593
1 1 1 2 3 1 3 2 1 2 1 2 2 3 1 1 2 2 3 2 3 1 2 3	594
1 1 2 2 1 3 1 1 3 2 1 1 3 2 1 3 1 3 2 2 2 1 1 3	595
2 3 2 1 1 3 2 2 2 1 1 1 3 2 1 1 3 1 1 1 2 3 2 3	596
3 1 1 1 2 3 1 2 1 1 3 2 2 3 1 2 1 2 1 1 3 1 1 3	597
1 1 2 3 1 3 2 1 3 2 2 2 3 2 1 2 2 2 3 1 3 2 2 2	598
1 3 2 3 1 1 2 3 2 1 1 3 1 2 2 1 2 3 2 1 2 2 2 3	599
3 2 1 1 2 2 3 1 1 2 2 3 1 1 1 3 1 2 1 1 3 2 3 2	600
2 1 2 3 2 2 2 1 1 3 2 1 3 2 3 1 1 1 2 1 3 1 3 2	601
3 2 1 2 2 3 1 1 1 2 2 3 1 1 2 2 1 3 1 1 3 2 1 3	602
1 1 2 1 2 3 2 1 1 2 3 2 1 3 2 2 3 1 1 1 3 2 3 1	603
2 3 1 1 2 1 2 2 3 1 3 1 1 2 2 1 2 3 1 3 1 3 2 2	604
2 1 3 2 3 2 1 1 1 2 3 1 2 3 1 1 3 1 1 1 3 2 1 2	605
3 2 1 2 3 2 3 2 1 1 1 3 1 1 1 2 2 2 3 1 2 3 2 1	606
1 1 2 2 3 2 2 2 3 1 1 1 3 2 2 2 3 2 2 3 1 3 1 1	607
1 1 2 2 3 2 2 2 3 1 3 2 1 3 2 1 2 2 1 3 2 1 3 2	608
2 1 1 2 2 3 1 3 2 2 2 3 1 1 2 1 1 3 1 3 1 3 2 2	609
2 3 2 2 3 1 2 2 3 2 1 1 3 2 3 2 2 2 1 2 2 3 2 2	610
3 1 1 1 2 2 2 3 2 3 1 3 2 1 2 3 2 1 2 2 3 1 1	611
2 1 1 3 1 1 2 3 1 1 2 3 1 1 2 3 1 1 3 2 3 1 1 2 1 2	612
2 1 1 2 3 2 3 1 1 3 2 2 2 3 2 3 1 1 1 3 1 2 1 2	613
2 2 3 2 1 2 1 2 3 1 1 1 3 2 1 1 3 1 1 3 1 1 3 2	614
2 1 3 1 3 1 3 1 1 3 1 1 3 1 1 1 2 1 1 3 1 1 2 1	615
1 2 2 2 3 1 1 1 2 3 2 2 1 1 2 3 1 3 1 3 1 3 1 2	616
2 2 3 2 3 2 3 2 1 2 1 2 1 3 2 1 2 2 1 3 1 1 2 3	617
1 2 2 3 2 2 1 3 2 1 2 2 3 1 2 3 2 3 1 1 3 2 2 1	618
2 3 2 2 3 2 1 2 2 2 3 1 1 2 3 1 1 1 2 3 1 1 3	619
2 3 2 2 1 3 1 2 2 3 2 3 2 2 1 1 1 2 3 2 1 3 2 2	620
2 1 2 1 3 1 3 2 1 2 2 3 2 1 2 1 3 1 3 1 3 1 1 1	621
1 1 1 2 1 3 2 1 1 3 1 1 2 3 2 1 3 2 2 3 2 2 3 1	622
2 3 1 3 2 3 2 3 1 2 2 2 1 2 3 1 2 2 1 1 3 2 2 1	623
1 3 1 1 2 2 2 3 2 2 3 2 1 3 2 3 2 2 1 2 3 1 2 2	624
3 1 2 2 3 1 1 3 1 1 1 3 1 1 1 2 1 3 2 2 2 3 1 1	625
3 1 2 1 1 2 1 3 1 3 1 1 2 1 3 2 1 3 1 3 2 2 1 1	626
3 1 2 2 3 1 1 1 2 2 3 2 1 3 2 2 1 2 1 3 2 3 1	627
3 1 2 2 2 1 1 3 1 1 3 1 2 3 1 1 2 1 1 2 3 2 1 3	628
2 2 2 3 1 3 1 3 1 1 1 3 2 1 3 1 1 2 1 1 3 1 2 1	629
3 1 2 2 1 1 3 1 3 2 1 1 1 2 3 1 3 2 1 2 1 1 3 1	630
2 2 2 3 1 2 1 3 1 1 2 2 3 1 1 1 2 2 2 3 1 3 1 3	631
2 3 1 1 3 1 1 3 1 3 2 3 2 2 1 2 1 1 3 1 2 2 2 1	632

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
3 2 3 1 1 1 2 3 1 2 2 2 1 3 1 3 2 1 1 2 1 1 3 2	633
1 1 1 2 1 1 3 1 1 2 1 3 1 3 1 3 1 1 1 3 2 2	634
3 2 2 3 2 1 1 1 3 2 1 1 2 1 3 1 3 1 1 1 2 2 1 3	635
1 3 2 3 1 2 2 2 1 3 1 2 2 1 2 3 2 3 1 2 3 1 2 2	636
1 3 1 3 2 1 2 1 3 2 2 2 1 3 1 2 2 2 1 2 3 2 1 3	637
1 2 3 1 2 2 1 3 1 2 1 3 2 3 1 1 1 2 2 3 2 2 1 3	638
1 2 3 1 1 1 2 3 2 1 2 2 1 3 2 2 2 1 3 1 3 2 2 3	639
1 2 1 2 2 3 1 3 2 3 1 3 1 3 2 2 1 2 2 3 2 2 1 1	640
1 3 1 2 3 2 3 2 1 2 2 3 1 1 2 2 1 1 3 1 1 3 2 2	641
2 1 1 2 3 2 3 2 2 3 1 2 1 3 1 1 2 1 3 1 3 1 2 1	642
1 1 1 2 2 1 3 2 2 3 1 1 1 3 2 1 2 3 1 3 1 1 1 3	643
2 2 2 1 3 1 3 2 2 3 1 1 3 1 1 1 2 3 2 2 1 1 2 3	644
3 1 2 2 3 2 2 3 1 2 2 1 2 2 3 1 2 3 1 1 2 2 2 3	645
2 3 2 2 3 2 2 3 2 2 3 1 1 2 2 3 1 1 3 1 1 2 2 1	646
1 2 2 1 1 3 2 1 1 3 1 1 2 2 3 1 3 1 3 2 2 2 3 1	647
3 2 1 2 3 2 2 3 2 1 1 2 3 2 1 2 2 1 1 3 1 1 1 3	648
2 1 3 2 2 3 2 3 1 2 2 2 1 2 3 2 1 1 2 3 1 2 2 3	649
2 3 1 2 1 1 2 3 1 1 1 3 2 2 2 1 2 1 3 1 3 1 3 1	650
3 2 1 1 3 1 2 2 3 2 2 2 3 2 1 2 3 1 2 1 1 3 1 2	651
2 2 3 1 1 2 2 1 1 3 1 3 2 1 1 3 1 2 3 2 2 2 1 3	652
1 1 3 2 3 2 2 2 3 2 2 2 1 3 1 3 2 1 1 1 3 1 2 1	653
1 3 1 3 1 3 1 2 1 1 1 3 2 1 2 1 3 1 1 3 2 2 1 1	654
1 2 2 1 2 3 1 1 2 1 3 2 2 1 3 1 1 1 3 1 3 1 3 2	655
2 2 3 2 2 3 1 2 1 2 2 1 3 1 3 1 1 2 3 2 3 2 2 2	656
2 2 2 1 2 2 3 1 3 1 3 2 2 2 3 2 2 1 2 2 2 3 2 3	657
1 3 2 3 2 2 1 1 3 1 1 3 2 2 3 1 2 2 1 2 2 3 1 2	658
3 1 3 1 1 2 3 1 2 2 3 1 1 2 3 2 2 3 1 2 1 1 2	659
3 1 2 1 1 3 2 1 2 2 1 3 2 1 2 3 1 3 2 3 2 1 1 2	660
2 2 2 3 1 2 2 2 1 1 3 1 3 2 3 2 2 3 1 1 2 3 2 1	661
1 1 3 2 2 1 3 2 1 1 1 2 1 3 1 3 2 1 3 1 1 1 3 1	662
3 2 1 1 1 3 2 1 2 3 1 1 2 1 2 3 2 3 1 1 1 2 3 2	663
2 1 1 2 1 1 3 2 3 2 3 2 2 3 2 3 1 1 2 3 2 1 1 2	664
1 1 1 3 1 2 2 2 1 3 1 3 2 1 3 1 1 1 3 1 3 1 1 2	665
2 2 1 3 2 2 2 3 1 3 2 2 3 1 1 1 2 1 3 2 1 1 1 3	666
2 1 1 2 1 3 2 1 2 3 1 3 2 1 1 3 1 2 2 3 1 1 1 3	667
3 1 1 3 1 2 2 1 3 1 2 2 3 1 2 3 2 2 1 3 2 2 1 1	668
2 1 1 1 3 1 3 1 3 1 1 3 2 2 1 3 2 1 1 2 1 3 1 1	669
2 1 1 3 2 1 2 3 1 3 1 1 1 2 3 1 2 3 2 3 2 2 1 2	670
3 1 3 2 2 2 3 2 2 2 3 2 2 1 3 2 2 1 2 2 3 1 2 1	671
1 1 3 2 1 1 1 3 1 1 1 2 3 2 2 1 1 3 1 3 2 1 3 2	672
1 2 3 1 3 1 1 2 2 3 2 2 3 2 2 3 1 1 1 2 3 2 1 1	673
2 2 1 3 1 2 2 1 3 1 3 2 1 3 2 1 3 1 1 3 1 1 2 1	674
2 1 3 2 3 1 2 3 1 1 3 1 1 3 2 2 1 3 1 1 1 2 2 1	675
2 1 1 2 3 2 1 3 2 1 1 2 3 2 3 1 2 3 1 2 1 1 3 2	676
2 2 3 1 3 1 1 1 3 1 1 2 1 1 3 2 1 3 2 3 2 1 1 1	677
2 1 1 2 3 1 3 2 3 1 3 1 2 2 1 2 1 3 1 2 2 3 2 2	678
3 2 1 2 1 1 3 1 1 1 2 3 2 3 2 3 2 2 2 3 1 2 2 1	679
3 2 3 1 1 2 3 2 3 2 2 1 1 2 3 1 1 3 1 2 1 2 1 2	680
3 1 1 1 3 2 2 1 2 2 1 3 2 2 1 3 2 2 1 1 1 3 1 2 3	681
2 1 3 1 1 2 2 3 2 3 2 2 3 1 2 1 1 3 2 3 1 2 1	682
2 3 1 2 2 2 1 3 1 2 2 3 1 3 1 3 2 2 1 1 1 2 3 1	683
1 2 2 1 2 2 3 1 3 2 2 2 3 1 1 2 3 2 2 3 1 2 1 3	684
1 2 1 3 2 1 3 2 2 1 2 3 2 2 2 3 1 2 2 2 1 3 2 3	685
1 2 1 3 1 1 3 1 1 3 1 1 2 1 1 1 3 2 2 1 3 1 3 1	686
3 1 2 3 2 2 3 1 1 1 3 2 1 1 2 3 1 1 2 2 2 3 2 1	687
3 1 3 1 2 2 3 1 2 1 3 2 1 3 1 1 1 2 3 1 2 1 1 1	688

Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern	Sequence Identifier
2 3 1 3 1 3 1 1 2 1 1 1 3 2 1 2 3 1 1 2 2 2 3 1	689
2 1 2 1 1 1 3 1 2 3 1 2 3 2 3 1 1 2 2 1 3 2 1 3	690
2 2 1 2 3 2 1 1 3 1 1 2 3 2 2 2 3 1 3 1 3 1 1 1	691
1 3 2 1 1 1 2 3 1 2 3 1 1 2 3 1 2 1 2 3 1 2 3 1	692
3 1 1 1 2 2 2 3 2 3 2 2 1 1 1 3 2 2 3 1 1 2 3 1	693
3 1 2 3 1 1 2 3 1 2 2 3 2 3 2 2 2 1 1 3 2 1 2 1	694
3 1 1 1 2 1 1 3 2 3 1 3 1 3 2 2 1 1 2 3 1 1 1 2	695
2 3 2 2 3 1 1 1 2 1 3 2 2 1 2 2 1 3 2 2 2 3 2 3	696
2 2 2 3 1 3 1 3 2 1 2 1 2 2 3 1 2 1 2 3 1 3 1 1	697
1 2 2 3 2 3 2 3 2 1 1 1 3 2 1 1 3 1 2 2 2 1 1 3	698
2 1 2 1 3 2 2 2 3 1 1 3 2 3 2 3 1 2 3 2 1 2 2 2	699
3 2 3 1 1 3 2 2 1 2 1 3 2 3 2 1 2 1 1 1 3 1 1 2	700
3 2 1 2 3 2 2 3 1 1 2 1 3 2 1 1 1 2 1 3 1 2 2 3	701
2 2 1 3 1 1 3 2 3 2 3 1 2 2 2 3 2 3 2 1 2 2 2	702
2 2 2 1 3 2 1 1 2 1 2 3 2 1 1 3 1 3 1 2 3 2 3 1	703
1 3 2 1 2 3 2 1 2 1 3 1 2 3 1 2 3 2 2 2 3 2 2 2	704
1 2 2 2 1 1 3 2 1 1 1 3 2 3 2 1 3 1 3 1 2 1 1 3	705
1 2 2 2 3 2 3 2 2 3 1 1 2 2 3 2 1 1 1 3 2 3 1 1	706
1 2 3 2 2 1 2 2 1 3 1 2 2 3 2 3 1 2 3 1 1 2 3 1	707
2 1 3 2 1 3 2 1 3 1 1 2 1 2 3 1 1 1 2 2 1 3 1 3	708
2 2 2 1 1 2 3 1 3 1 1 3 1 3 2 2 1 3 1 3 2 1 2 1	709
1 1 1 3 2 2 2 1 3 2 1 3 1 3 2 3 2 1 2 3 2 1 1 1	710
1 2 1 2 1 2 3 1 2 1 3 2 1 3 1 3 2 1 3 1 2 2 1 3	711
2 3 1 3 1 1 3 2 2 1 1 2 2 3 2 1 2 1 3 1 2 2 3 1	712
2 1 2 1 3 1 3 1 2 3 2 2 1 2 1 2 3 1 1 3 2 2 3 2	713
1 1 1 2 2 2 3 2 2 1 1 3 2 2 3 2 2 3 2 2 3 2 2 3	714
2 2 3 2 2 3 1 1 3 1 2 3 1 1 1 3 2 1 3 1 1 2 2 1	715
1 1 3 1 3 1 2 1 1 3 2 1 3 2 2 2 1 2 3 2 2 2	716
1 1 2 1 1 3 1 1 3 1 1 3 2 3 1 1 1 3 1 2 2 3 1 2	717
2 1 1 3 2 2 1 1 1 3 2 2 3 1 2 3 1 2 2 3 1 2 1 3	718
1 2 1 2 1 1 3 1 2 1 1 3 1 3 2 3 2 1 1 3 2 3 1 2	719
3 2 2 1 1 1 2 3 2 2 3 2 2 3 2 2 2 1 1 3 2 3 1 2	720
3 1 3 2 2 1 1 3 2 2 1 2 2 1 3 2 2 1 1 3 1 1 3 2	721
2 1 2 2 1 3 1 3 2 2 2 3 1 3 1 1 2 1 1 3 2 1 3 2	722
2 1 1 2 3 2 2 3 2 2 1 2 3 2 3 2 2 1 3 1 2 3 2 2	723
3 1 1 1 3 2 2 3 1 2 1 3 1 1 2 3 2 1 1 2 3 2 2 2	724
2 3 1 2 1 3 1 2 3 1 1 2 2 3 1 2 2 3 1 2 2 1 3 2	725
1 2 3 1 2 1 3 1 3 2 1 1 1 3 1 1 2 1 1 3 2 2 3 2	726
1 3 2 1 1 3 2 3 2 2 1 3 1 2 1 3 2 1 2 2 3 1 1 2	727
1 2 3 2 1 3 1 2 2 1 1 1 3 2 1 3 2 3 2 1 2 3 2 2	728
2 2 1 2 2 3 1 2 1 1 2 3 1 3 1 3 1 3 2 2 1 1 1 3	729
1 2 2 2 3 2 2 1 2 3 1 2 1 1 1 2 3 2 3 2 1 3 2 3	730
2 2 3 1 1 3 1 1 2 1 1 3 1 3 2 1 1 2 1 1 3 1 3	731
2 3 2 3 2 1 1 2 1 1 3 2 1 3 2 1 1 3 1 2 2 1 3 1	732
1 2 3 1 1 1 3 2 2 1 3 1 3 2 2 2 1 2 3 1 2 1 1 3	733
1 2 2 1 3 2 2 1 1 3 1 3 1 3 2 2 2 3 2 1 3 1 2 2	734
2 3 2 1 3 2 1 2 2 3 2 1 2 3 1 2 2 1 1 1 3 2 3 2	735
1 3 2 2 3 1 2 1 1 1 3 1 1 3 1 1 3 1 3 2 1 2 1 2	736
3 2 1 1 2 3 1 3 1 2 1 1 1 3 1 3 1 3 1 2 1 1 2 2	737
2 3 2 3 2 2 3 1 1 3 1 2 1 1 1 3 2 2 2 1 2 3 1 2	738
1 1 3 1 1 3 1 3 2 1 3 2 2 1 3 1 1 2 2 3 1 2 2 1	739
3 1 1 2 3 1 1 3 1 2 3 1 1 3 2 2 2 3 2 2 1 1 2 1	740
1 1 1 2 2 3 2 2 3 1 3 1 2 1 1 3 1 2 1 3 2 3 1 2	741
2 3 1 2 2 3 2 2 2 1 1 2 3 1 2 3 2 3 2 3 1 2 2 1	742
1 2 3 1 1 3 2 1 2 2 3 2 2 3 1 3 2 3 1 2 2 2 1 1	743
3 2 3 2 1 1 1 2 3 2 2 2 3 1 3 1 2 3 2 1 2 1 2 2	744

**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier	
1	1	2	2	3	1	2	3	1	3	2	2	2	1	1	1	3	1	3	2	2	3	1	2	745
2	2	2	3	2	3	2	1	1	2	1	2	3	1	2	2	3	1	3	1	3	2	2	2	746
3	2	1	3	2	1	3	1	2	3	1	2	2	1	1	3	1	1	3	1	2	1	1	1	747
2	2	2	1	1	2	3	2	3	1	1	1	2	2	2	3	2	2	3	2	3	1	3	2	748
3	2	1	1	1	3	1	1	2	2	1	3	1	2	1	1	1	3	1	3	2	3	1	2	749
1	1	2	1	3	2	2	1	1	3	2	2	2	1	1	3	1	3	2	2	3	2	3	2	750
3	2	3	2	3	1	2	3	2	2	2	1	2	1	3	1	2	2	2	3	2	2	1	2	751
3	2	1	2	1	3	2	3	2	3	1	2	2	1	3	1	2	2	2	3	2	1	1	1	752
3	2	2	3	2	1	1	3	1	1	1	3	1	2	1	2	3	2	1	1	3	1	1	1	753
1	2	1	2	2	1	3	1	2	2	3	2	1	1	1	3	1	3	1	3	2	3	1	1	754
3	1	3	2	3	1	2	1	2	2	3	1	1	1	2	2	1	3	1	2	2	3	2	1	755
2	1	1	3	1	1	3	2	2	1	1	1	3	1	1	3	1	3	1	3	2	2	2	1	756
3	1	2	3	2	2	1	3	1	2	1	1	1	3	2	2	2	1	1	3	2	1	3	2	757
3	2	3	1	2	2	3	2	1	2	3	1	3	1	1	1	2	3	2	2	1	1	1	2	758
2	3	1	2	2	1	2	2	3	2	1	1	3	1	1	1	3	1	2	2	3	1	3	1	759
1	1	3	1	1	2	2	3	2	3	2	1	1	3	2	2	2	1	2	3	1	3	2	1	760
2	2	3	2	1	2	2	2	1	3	1	1	3	1	2	2	2	3	2	1	3	1	2	3	761
2	1	2	1	2	3	2	2	2	3	2	3	2	1	1	3	1	1	3	1	1	1	2	3	762
3	1	2	1	1	2	3	2	3	2	3	1	1	2	2	2	3	2	3	1	1	2	1	1	763
2	2	1	3	1	1	1	2	3	2	3	1	3	1	2	2	2	2	1	1	3	1	3	2	764
1	3	2	3	2	1	3	1	1	2	2	2	3	2	1	2	2	2	1	3	2	2	3	2	765
2	1	3	2	2	1	1	3	1	2	1	3	1	3	2	1	1	1	2	3	1	2	1	3	766
3	1	1	3	2	3	1	2	1	2	2	3	2	1	1	1	2	2	3	1	2	1	1	3	767
3	2	1	1	2	2	3	2	3	2	2	1	3	1	2	2	2	1	1	3	1	1	3	2	768
2	3	1	2	1	2	2	3	2	3	1	1	2	2	3	1	2	1	3	2	1	2	3	769	
1	1	3	2	1	1	1	3	1	3	1	2	1	2	1	3	2	2	1	1	3	2	2	3	770
1	2	2	1	3	2	2	1	1	3	2	2	1	2	2	2	3	2	3	1	3	2	3	1	771
1	3	1	2	3	1	1	3	2	1	3	2	2	2	1	2	3	1	1	2	2	1	3	1	772
2	3	1	3	2	2	1	3	2	2	1	1	3	2	3	1	2	1	3	2	2	1	1	1	773
2	2	1	2	2	3	2	1	3	1	2	2	2	1	3	1	3	1	1	3	1	2	3	1	774
2	1	2	2	2	3	2	3	2	2	2	3	2	2	3	1	2	2	1	3	1	2	1	3	775
3	2	1	2	1	1	2	3	2	3	2	3	2	3	1	1	1	3	2	2	1	2	1	1	776
2	1	2	1	2	3	2	2	3	1	3	2	1	2	1	1	1	3	1	3	1	3	1	1	777
2	2	1	3	2	2	1	3	2	2	2	1	1	1	3	1	2	2	3	2	3	1	3	2	778
2	2	2	1	3	1	1	2	1	1	3	2	3	1	2	3	2	3	1	2	3	1	1	1	779
1	3	1	3	2	1	1	2	3	2	3	2	1	1	1	2	1	3	2	2	1	3	1	2	780
2	3	2	3	1	2	1	1	1	3	1	3	1	1	1	2	2	1	3	2	2	3	2	2	781
3	1	1	2	2	2	1	3	2	3	1	1	2	3	2	2	2	3	1	3	1	2	2	1	782
2	3	2	3	1	2	3	2	3	2	1	1	3	2	1	2	1	2	3	1	1	1	2	2	783
2	2	3	2	3	1	1	2	3	1	2	2	1	1	2	3	1	1	2	1	3	1	1	3	784
1	1	2	3	2	2	3	2	2	2	1	3	1	2	2	3	1	3	1	1	1	3	2	2	785
1	3	1	2	2	3	2	3	2	2	1	3	2	1	2	2	1	3	2	1	2	1	1	3	786
2	2	3	1	2	3	2	1	2	2	1	3	1	1	1	3	2	2	2	1	2	3	2	3	787
2	1	2	3	1	2	2	3	2	3	2	3	2	2	1	3	1	3	1	1	2	2	2	1	788
2	1	3	2	3	2	1	3	1	2	1	2	2	2	3	1	2	1	3	2	2	1	2	3	789
1	3	2	2	2	1	1	2	3	2	3	2	2	2	1	3	2	2	3	2	2	1	2	3	790
2	3	2	3	2	1	1	1	3	2	1	3	1	1	1	3	2	1	1	1	3	1	2	2	791
3	2	2	1	2	3	1	2	1	2	1	3	2	3	1	3	2	2	3	2	2	1	2	2	792
2	2	2	3	1	2	2	3	1	1	2	3	2	2	1	1	2	1	3	2	2	3	2	3	793
1	3	1	3	2	1	2	2	1	3	2	1	3	2	2	1	2	2	3	2	1	1	3	2	794
2	1	1	3	2	1	3	1	1	1	3	1	1	3	1	1	3	1	2	1	2	2	2	3	795
1	3	1	1	1	3	1	3	1	1	2	2	1	2	3	2	1	1	2	3	1	1	1	3	796
2	2	1	3	1	2	2	2	3	2	2	1	3	2	3	2	3	1	2	2	2	1	1	3	797
3	1	2	3	1	2	2	1	1	3	1	2	1	2	1	3	1	3	1	2	1	3	2	2	798
1	2	1	2	2	2	3	1	3	2	3	1	2	2	1	1	3	1	3	2	1	1	2	3	799
2	3	2	1	2	2	3	2	3	1	3	2	2	1	1	3	2	1	2	1	1	3	2	2	800



**Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier		
1	1	2	2	2	1	3	2	1	3	1	1	1	3	2	3	2	2	3	2	3	2	2	2	801	
3	2	2	1	3	1	1	3	1	2	2	1	1	3	2	2	3	1	1	2	1	1	2	3	802	
2	1	1	1	3	2	1	2	3	2	3	1	3	1	2	3	1	2	2	2	1	2	3	2	803	
2	3	1	1	1	2	3	1	2	2	1	1	1	3	1	2	3	1	1	3	1	2	3	1	804	
2	2	1	2	2	1	3	1	2	3	2	2	3	1	3	2	3	2	2	2	3	2	2	2	805	
2	1	3	2	3	2	2	2	1	1	1	3	1	3	2	1	3	2	1	2	1	2	3	1	806	
1	3	2	2	1	2	1	1	3	2	1	1	1	2	3	1	2	3	2	2	3	1	2	3	807	
2	2	1	1	3	1	3	1	3	1	1	1	2	1	1	3	2	3	2	1	2	2	3	2	808	
3	1	2	1	2	2	3	1	1	1	2	3	2	3	2	2	1	1	1	2	3	1	2	3	1	809
1	2	3	1	2	3	1	1	2	2	1	1	3	1	1	1	3	1	1	1	3	1	3	1	810	
3	1	1	2	1	3	2	2	2	2	3	1	2	2	2	3	2	3	2	2	3	2	2	1	811	
1	3	2	2	3	2	2	2	1	3	1	2	2	2	3	1	2	2	2	3	2	1	1	3	812	
3	2	1	2	3	1	3	1	2	2	2	3	1	2	1	2	1	1	3	1	2	2	1	3	813	
2	2	2	1	2	1	3	2	3	1	3	2	1	2	1	3	2	3	1	2	3	1	2	2	814	
2	1	2	1	2	3	2	3	1	1	3	1	2	1	2	1	1	3	2	3	2	2	2	3	815	
1	2	2	3	1	2	1	3	1	2	3	1	2	1	3	2	1	1	2	2	3	1	3	2	816	
2	3	1	2	1	3	1	2	3	2	3	1	1	3	1	1	2	2	2	3	1	2	2	2	817	
3	1	1	3	1	2	1	2	2	3	1	1	1	3	1	1	2	2	2	3	1	2	3	2	818	
3	1	2	3	2	2	2	1	3	2	3	2	1	3	1	2	1	2	1	3	1	2	2	2	819	
3	1	1	2	1	2	2	3	1	3	2	2	1	2	1	1	3	2	1	3	2	1	3	2	820	
1	3	2	3	1	3	2	1	1	3	2	1	1	2	1	3	1	1	1	3	1	2	2	2	821	
3	2	1	3	1	1	2	1	1	3	2	1	1	2	2	2	3	2	3	1	3	1	2	1	822	
3	1	3	2	2	1	2	2	2	3	1	3	1	2	2	2	1	3	1	2	3	2	2	2	823	
3	1	1	1	2	3	1	2	3	1	2	2	3	1	1	2	2	2	1	3	1	3	1	2	824	
1	1	1	2	1	3	2	3	2	3	1	3	1	1	2	1	3	2	2	1	1	3	2	1	825	
1	2	3	2	3	2	2	1	1	3	2	2	3	2	1	3	1	1	3	1	1	2	1	1	826	
1	2	1	1	2	3	1	3	2	2	1	1	2	1	3	2	3	2	1	1	3	1	1	3	827	
1	2	1	1	3	1	3	1	2	3	2	2	2	1	1	3	2	2	1	3	1	1	1	3	828	
2	3	2	2	1	3	2	3	2	2	1	3	1	1	1	2	1	2	3	1	1	1	3	1	829	
2	2	2	1	3	1	1	3	1	2	2	3	2	2	1	3	1	2	1	1	3	2	2	3	830	
3	2	3	2	1	1	2	3	2	1	2	1	1	3	1	2	1	3	2	2	1	1	3	2	831	
2	1	2	2	1	3	1	3	1	3	1	1	1	2	2	3	2	1	3	1	3	1	2	2	832	
2	1	3	2	3	1	3	1	2	1	1	1	3	2	1	1	1	3	2	2	2	1	2	3	833	
2	2	3	2	3	1	1	1	3	2	2	1	1	3	2	1	1	3	2	2	1	3	2	2	834	
1	1	1	3	2	3	2	1	1	3	2	2	3	1	1	3	1	1	2	1	2	2	3	1	835	
3	1	1	2	1	3	1	3	2	3	2	2	1	2	2	2	3	1	1	1	2	1	3	1	836	
2	1	2	1	1	3	1	3	1	3	1	3	1	2	1	1	3	2	1	1	2	1	1	3	837	
2	3	1	3	2	3	1	1	1	2	2	3	1	2	1	3	1	3	2	1	1	1	2	2	838	
3	1	2	3	1	1	2	1	1	3	2	2	2	1	1	3	2	3	1	3	1	1	1	2	839	
3	2	3	2	3	1	2	1	2	3	2	2	2	1	2	2	3	1	2	2	1	1	3	2	840	
2	1	1	1	3	2	3	1	3	2	3	2	1	1	1	2	3	1	2	1	1	2	3	1	841	
3	2	1	3	1	3	2	2	2	3	1	2	2	2	3	1	1	1	3	1	1	2	1	2	842	
3	1	1	2	1	2	2	3	2	2	1	2	3	2	2	2	3	2	2	1	2	3	1	3	843	
3	2	3	2	1	1	2	1	1	3	1	2	3	2	1	2	2	3	2	2	3	2	2	2	844	
2	1	1	1	2	2	3	1	2	2	3	2	3	1	3	2	2	3	1	1	3	1	1	2	845	
2	3	1	3	1	2	1	3	2	2	1	2	1	3	2	2	1	1	3	2	2	2	1	3	846	
1	3	2	2	2	3	2	2	1	1	3	1	2	2	1	2	3	2	1	3	1	1	1	3	847	
3	1	1	2	3	2	3	2	1	3	1	1	2	1	1	3	1	3	1	2	2	1	1	1	848	
3	2	1	2	2	1	2	3	1	1	1	3	1	1	3	2	2	3	2	2	3	2	2	2	849	
3	2	3	2	2	1	2	1	3	1	1	3	2	2	1	1	1	2	3	2	2	1	1	3	850	
2	2	1	1	3	1	3	2	1	3	2	3	1	1	2	1	2	3	1	2	1	3	2	1	851	
1	1	2	3	2	2	1	2	1	1	3	1	2	3	1	3	1	3	2	2	2	1	3	2	852	
1	2	1	2	1	1	3	1	2	2	2	3	1	2	3	2	1	3	2	3	2	1	3	2	853	
2	1	2	3	2	2	2	3	2	2	3	2	2	3	2	2	1	1	3	2	2	2	3	1	854	
3	1	2	1	3	2	2	2	1	3	2	1	2	1	3	1	1	3	1	2	1	1	1	3	855	
3	2	2	3	1	1	2	1	2	1	3	1	3	1	2	1	3	2	1	1	1	2	1	3	856	

**Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides**

Numeric Pattern																							Sequence Identifier	
1	3	1	3	1	1	3	1	2	2	2	1	3	2	1	1	3	1	1	2	3	1	2	1	857
2	3	1	1	2	3	1	3	1	1	1	3	1	2	1	2	2	3	1	3	2	1	2	2	858
2	3	1	1	3	1	2	2	1	2	1	3	2	1	3	2	2	3	2	1	2	1	3	1	859
3	1	2	2	1	3	2	1	3	2	1	2	2	3	1	1	3	1	2	2	1	2	3	2	860
2	3	1	1	1	2	3	2	3	2	1	2	2	2	3	2	1	2	3	2	2	2	1	3	861
1	2	2	1	1	1	3	2	2	3	1	2	1	2	3	1	1	1	3	1	1	3	2	3	862
1	1	2	3	2	1	3	1	3	1	2	2	3	2	1	3	2	3	1	1	2	1	2	2	863
2	2	1	2	2	2	3	2	2	3	1	3	2	3	2	1	1	1	2	3	2	3	1	2	864
1	2	3	2	1	1	2	2	3	2	3	1	1	2	1	1	2	3	2	1	2	3	2	3	865
3	1	2	2	2	3	2	1	2	1	3	1	3	1	2	2	1	3	2	1	1	3	2	1	866
1	1	2	1	2	2	3	2	2	3	2	2	2	1	3	1	3	1	1	1	3	1	1	3	867
1	2	3	1	2	3	1	2	3	2	1	2	2	2	3	2	1	1	1	3	1	3	2	1	868
1	1	2	3	2	1	2	2	2	3	2	3	2	3	1	2	2	3	2	3	2	1	1	1	869
1	3	2	3	2	2	1	2	3	1	1	3	1	1	2	1	3	2	1	1	3	1	1	2	870
3	2	2	1	2	3	2	1	3	1	3	1	2	3	1	1	1	3	1	1	1	2	2	1	871
3	2	2	2	3	2	1	2	2	1	3	1	2	1	1	1	2	3	1	3	2	2	3	2	872
2	3	1	2	2	2	1	2	3	1	3	1	2	2	1	1	3	1	3	1	1	1	3	1	873
2	2	2	3	2	3	2	3	2	2	1	2	2	3	2	1	1	2	2	3	1	3	1	2	874
3	1	2	3	2	3	2	3	1	2	1	2	3	1	2	2	1	1	1	3	1	1	1	2	875
1	3	1	2	2	1	2	1	3	1	2	2	2	3	2	1	3	1	3	1	1	1	3	2	876
3	1	1	3	1	3	2	1	2	3	2	1	1	2	1	3	2	1	2	2	3	2	1	2	877
2	2	2	3	2	1	1	2	3	2	2	3	2	2	3	1	3	2	2	2	1	1	3	1	878
1	3	2	1	1	1	2	1	3	2	1	3	2	1	2	3	1	1	2	1	1	3	1	3	879
3	1	1	2	3	2	2	3	1	1	2	2	3	1	1	1	2	1	2	3	1	3	2	2	880
1	3	2	1	3	2	2	1	1	2	2	3	1	2	1	3	2	1	1	3	2	2	2	3	881
1	3	2	3	2	1	1	1	3	1	1	1	2	3	1	1	2	3	1	1	2	1	1	3	882
2	3	2	2	1	3	1	2	1	2	2	2	3	2	3	1	1	1	2	3	2	3	1	1	883
2	3	2	1	2	3	2	2	3	1	3	2	2	2	3	1	1	2	2	3	2	2	1	2	884
2	3	1	3	2	3	1	1	2	2	1	3	2	2	1	2	3	2	2	3	2	2	1	2	885
3	1	1	3	1	1	1	3	1	1	1	2	3	1	3	1	1	1	3	1	2	2	1	2	886
2	2	1	1	3	2	1	1	3	2	2	3	2	3	2	2	3	1	2	1	2	2	1	3	887
1	2	3	1	2	3	2	3	2	2	2	3	1	2	2	2	3	1	1	2	2	3	1	1	888
1	1	3	2	1	1	3	2	3	1	1	1	2	2	3	2	2	3	2	2	3	3	1	1	889
1	2	3	1	1	3	2	3	2	1	1	1	3	2	2	2	3	1	1	1	3	1	1	1	890
1	3	1	3	1	3	2	1	1	3	1	2	1	1	2	2	3	2	1	2	1	3	2	1	891
2	2	2	1	2	3	1	3	1	2	1	3	1	2	3	1	1	1	2	1	1	3	2	3	892
1	3	1	1	1	2	2	1	3	2	1	3	2	1	1	2	3	1	2	2	2	3	2	3	893
3	1	2	2	2	3	1	3	1	2	2	3	1	1	2	3	1	3	1	1	2	1	2	1	894
3	1	2	2	1	3	1	1	1	3	1	2	3	1	1	2	1	1	3	1	2	3	1	2	895
2	1	3	1	2	1	3	1	1	1	3	2	1	2	1	2	3	2	3	2	1	3	2	2	896
3	1	1	3	1	2	1	3	2	1	1	1	3	2	2	1	1	1	3	2	1	1	3	2	897
1	1	1	2	3	2	3	2	3	2	2	2	1	3	2	1	3	2	2	3	2	1	1	1	898
2	2	3	2	2	3	1	1	3	2	1	1	3	1	3	1	2	3	1	1	2	1	1	1	899
2	1	2	2	2	3	1	3	1	3	1	1	1	3	1	1	1	3	1	3	2	2	2	1	900
2	1	2	2	2	1	3	2	3	1	2	3	1	1	2	2	2	3	2	3	1	2	3	2	901
2	2	1	2	1	3	2	3	1	2	3	1	2	3	1	2	1	1	3	2	2	3	1	2	902
2	1	1	1	3	1	2	1	1	2	2	3	2	1	3	1	1	1	3	2	1	3	2	3	903
3	2	2	2	1	3	2	1	2	3	1	2	1	2	2	3	2	3	2	3	2	1	1	1	904
3	2	3	2	2	3	2	3	1	1	2	1	1	3	1	2	2	3	1	1	1	2	1	2	905
1	1	1	3	1	1	1	3	2	1	2	1	1	1	3	2	3	1	3	1	2	1	3	1	906
2	1	2	2	2	3	2	1	1	3	1	1	3	2	3	2	1	3	1	2	1	2	2	3	907
2	1	3	1	1	3	1	2	3	1	1	1	2	2	3	2	3	1	2	2	2	3	2	2	908
1	2	1	1	2	1	3	2	1	1	3	2	3	1	1	2	3	1	2	3	1	3	1	2	909
1	1	2	3	2	3	1	1	2	1	1	3	1	2	1	1	1	3	2	3	2	3	2	1	910
1	2	2	3	1	1	3	1	2	1	1	1	3	1	2	3	2	2	3	2	2	2	1	3	911
2	3	1	1	1	2	1	3	1	1	3	2	3	1	3	1	2	2	1	2	1	3	2	1	912

Table IA: Numeric sequences corresponding to nucleotide  
base patterns of a set of oligonucleotides

Numeric Pattern																								Sequence Identifier
1	3	2	2	1	2	2	3	2	3	1	1	1	3	1	3	2	2	2	1	2	3	1	2	913
1	1	1	2	1	3	2	1	3	2	3	1	2	1	3	1	3	1	1	3	1	2	2	2	914
1	3	2	3	2	1	2	3	1	1	3	2	3	2	1	1	2	1	1	3	1	2	2	1	915
2	3	1	2	2	1	1	3	1	2	2	3	2	3	2	1	3	2	3	2	2	1	2	1	916
1	3	2	2	2	1	2	3	1	2	1	2	2	3	2	1	3	1	2	3	1	3	2		917
2	1	2	3	2	3	2	1	2	3	1	1	3	1	2	2	1	2	1	3	2	2	1	3	918
3	1	1	1	2	2	3	2	2	3	2	1	2	1	3	1	3	2	3	1	2	1	2	1	919
2	1	3	1	1	1	2	1	3	2	2	2	1	1	3	2	1	2	1	3	2	3	2	3	920
2	3	1	2	2	2	1	3	1	2	3	2	2	2	1	2	2	3	2	3	1	3	1	1	921
1	1	3	2	2	3	1	2	1	2	2	2	3	2	2	3	2	2	1	3	1	2	3	1	922
2	3	1	2	3	2	3	1	2	1	1	2	3	1	3	1	1	2	1	1	1	3	1	1	923
1	1	1	3	2	2	2	1	3	2	2	2	3	2	1	2	2	1	3	2	1	3	1	3	924
1	3	2	2	2	3	1	2	3	2	3	1	2	1	3	2	1	1	1	2	1	3	1	1	925
1	1	3	2	3	2	2	1	2	2	3	1	1	2	3	2	3	1	2	3	2	2	1	2	926
1	1	1	2	2	3	1	1	3	2	3	2	3	1	2	1	1	2	3	2	2	2	3	2	927
3	2	2	2	1	3	2	3	1	2	2	1	1	1	3	1	2	1	3	1	2	2	1	3	928
1	2	1	1	3	2	3	2	1	2	1	1	3	1	3	1	1	3	2	3	2	2	1	1	929
1	2	3	1	1	2	2	2	3	2	2	2	3	2	3	1	2	3	1	1	3	2	2	1	930
1	1	1	3	1	1	2	2	3	1	3	1	1	1	2	3	1	1	1	3	2	2	1	3	931
1	3	2	3	2	1	1	3	1	3	2	1	2	1	1	1	3	2	1	2	2	2	3	1	932
3	1	1	2	2	1	1	3	1	2	2	3	2	2	1	2	1	2	3	2	3	1	3	2	933
2	1	2	3	1	1	1	3	2	3	2	2	3	2	2	2	1	1	3	2	1	1	3	1	934
2	1	1	1	3	2	1	1	1	2	3	2	2	1	2	3	2	3	1	3	1	3	1	1	935
1	1	1	3	1	2	1	2	2	3	1	2	2	3	1	3	1	2	1	3	1	3	2	2	936
1	1	3	2	3	1	2	1	2	3	1	1	2	1	2	3	2	3	1	3	1	1	1	2	937
1	1	1	2	1	3	1	3	2	2	2	3	2	2	1	1	2	3	2	1	1	3	2	3	938
3	1	2	2	2	1	3	1	2	3	1	3	2	2	1	1	3	1	1	2	2	2	1	3	939
2	2	3	2	1	1	1	2	3	1	3	2	3	2	3	1	1	2	1	2	2	3	2	1	940
1	3	2	1	3	2	3	2	1	2	2	3	1	3	1	2	1	1	2	1	3	1	1		941
2	3	1	3	2	2	1	1	1	3	1	3	2	2	3	2	2	3	1	2	1	2	2	2	942
1	1	1	3	1	3	2	3	2	1	2	2	1	3	1	1	1	2	1	3	2	2	2	3	943
3	2	2	2	1	3	2	2	1	2	2	2	3	1	2	3	1	3	1	2	1	1	2	3	944
1	1	3	2	3	2	1	1	1	2	3	1	1	2	1	1	1	3	1	3	2	2	3	2	945
1	1	2	1	1	1	3	2	3	1	3	2	1	3	1	1	3	2	3	2	1	1	2	2	946
2	1	2	2	3	1	3	2	2	2	3	2	3	2	1	1	1	3	1	1	3	1	2	1	947
2	2	2	1	2	1	3	2	2	3	2	2	3	2	2	3	1	1	1	3	2	2			948
1	2	3	1	1	1	2	1	2	3	1	2	2	3	2	3	2	2	2	3	2	2	3	2	949
1	1	1	3	1	3	1	2	3	2	1	1	1	3	2	3	1	3	2	2	1	2	2	1	950
2	2	3	1	1	3	1	1	1	3	2	2	1	3	1	2	3	1	2	3	1	1	2	2	951
1	2	3	2	2	1	2	2	2	3	2	2	2	1	3	2	2	2	3	2	3	2	3	1	952
1	1	1	2	1	2	3	1	1	2	2	2	3	1	1	3	1	3	1	1	3	2	3	1	953
3	1	2	2	1	3	1	2	1	2	1	3	1	1	2	1	2	2	3	1	1	3	1	3	954
2	2	1	3	1	1	2	1	1	3	1	3	1	1	1	2	3	2	1	2	3	2	3	2	955
2	2	2	1	2	3	1	1	1	3	1	3	1	1	3	2	3	2	1	2	2	1	2	3	956
3	2	1	1	3	2	1	2	2	1	1	3	2	3	2	3	1	2	2	2	1	3	2	1	957
1	2	1	1	1	3	1	3	1	1	3	2	1	1	1	3	1	3	2	1	1	1	3	2	958
1	2	2	3	2	2	1	1	2	2	3	1	1	3	2	3	2	1	2	3	1	1	1	3	959
2	1	2	1	2	1	3	2	2	3	1	3	2	2	3	1	3	2	1	1	3	1	2	2	960
2	1	3	1	2	3	1	3	1	2	1	2	1	2	3	1	1	1	3	1	2	1	3	2	961
1	2	1	1	3	1	1	3	1	2	3	1	2	2	2	3	2	3	2	1	1	1	2	3	962
2	2	1	3	2	1	1	2	1	1	3	1	1	1	3	1	2	3	1	1	3	1	3	1	963
3	1	2	2	2	3	2	3	1	3	2	2	1	1	1	3	2	1	1	1	2	1	3	1	964
1	1	1	2	1	3	1	2	3	2	1	3	1	1	2	2	2	3	2	3	2	3	2	2	965
3	1	1	1	2	2	1	3	2	3	2	2	2	3	2	3	2	3	2	1	2	2	1	2	966
1	2	2	2	3	1	3	2	1	2	3	1	2	1	3	1	1	3	1	2	2	3	2	2	967
1	2	1	3	1	3	2	2	3	1	1	3	2	1	2	3	2	1	1	1	3	2	2	2	968

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern	Sequence
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Numeric Pattern																							Sequence Identifier	
2	1	1	2	2	2	3	2	3	1	1	2	3	2	2	3	2	2	1	2	2	3	2	3	969
2	2	1	3	2	2	2	1	2	3	1	3	1	3	2	3	1	3	1	2	2	2	1	1	970
3	2	2	3	2	2	1	3	1	3	2	3	2	2	2	1	2	3	1	1	1	2	2	2	971
2	2	2	1	2	2	3	2	3	1	2	3	2	3	1	1	1	2	1	1	3	1	3	1	972
3	2	1	1	3	2	1	1	2	1	2	3	1	2	1	3	2	3	1	2	2	1	1	3	973
2	3	1	3	1	2	3	1	2	3	2	1	2	1	2	3	2	1	3	2	1	1	2	1	974
1	1	2	2	3	1	3	1	1	1	3	1	3	1	2	1	1	1	2	3	1	2	1	3	975
2	2	2	3	1	1	3	2	3	1	2	3	2	2	1	3	1	1	2	3	2	2	2	1	976
1	3	2	2	3	2	2	3	2	3	2	1	1	2	2	3	2	2	1	3	2	1	1	1	977
1	2	1	3	2	3	1	3	1	1	3	2	3	1	2	1	1	3	1	2	1	2	2	2	978
3	2	3	2	3	1	2	1	1	3	2	1	1	2	2	3	1	3	2	2	1	1	1	2	979
2	1	3	2	2	1	2	2	3	2	2	2	3	2	3	1	2	2	2	3	1	3	1	1	980
1	2	1	3	2	2	3	1	1	2	1	3	2	1	1	2	2	2	3	1	1	3	1	3	981
1	2	3	2	2	2	3	2	3	2	2	2	3	1	1	2	1	3	1	3	1	1	2	1	982
2	3	1	2	1	1	1	3	1	2	1	2	3	1	3	1	3	1	2	2	3	2	1	1	983
2	1	1	1	3	1	2	3	1	3	1	2	3	2	2	3	2	2	1	1	1	3	2	2	984
1	1	3	2	3	1	1	1	2	2	2	3	2	1	1	3	1	1	2	2	1	3	2	3	985
3	1	1	1	2	3	1	3	1	3	2	2	1	2	2	3	1	2	1	3	2	2	2	1	986
2	2	2	3	2	1	1	1	2	3	1	3	1	2	1	2	1	3	2	3	2	2	1	3	987
3	2	2	1	1	2	2	3	2	3	1	2	1	2	2	2	3	1	2	2	1	3	2	3	988
1	3	1	3	2	3	2	2	3	1	2	1	1	1	3	1	2	3	2	2	2	1	2	1	989
1	1	2	2	3	2	3	1	3	1	1	1	2	2	3	1	2	1	1	3	1	1	3	1	990
2	2	1	1	1	3	1	3	1	1	2	2	3	1	3	1	1	3	1	3	1	1	1	2	991
2	2	3	2	2	1	3	1	1	3	1	1	2	2	3	1	1	2	3	2	1	2	3	2	992
1	3	2	2	1	1	3	1	2	1	2	3	2	3	2	3	1	2	3	2	2	2	1	1	993
2	3	1	3	2	2	1	2	3	2	2	3	2	1	1	2	1	3	1	1	1	2	2	3	994
2	2	1	3	1	2	1	1	3	2	2	2	1	3	1	3	1	2	2	3	1	3	1	1	995
1	2	3	1	3	2	1	1	2	1	1	3	1	3	2	1	2	2	2	3	1	1	3	2	996
2	3	2	2	2	1	1	3	2	3	2	1	1	2	3	1	2	2	2	3	2	2	1	3	997
2	2	3	1	1	3	1	1	3	1	2	2	3	2	2	1	2	2	3	2	2	3	1	1	998
2	1	2	1	3	1	1	1	3	1	2	2	1	1	1	3	1	3	2	3	1	1	2	3	999
2	1	1	1	2	2	3	2	2	1	3	1	1	1	2	2	2	3	1	3	2	3	2	3	1000
1	2	3	3	2	2	1	3	2	3	2	3	2	2	1	2	2	3	1	2	2	1	2	3	1001
3	1	3	1	1	2	2	1	2	3	2	3	2	3	1	1	2	1	2	1	3	1	1	1	1002
2	2	3	1	2	2	3	1	2	1	1	1	3	2	1	1	1	3	1	3	2	3	2	1	1003
3	2	3	2	3	2	1	1	1	2	2	3	1	1	2	1	2	3	2	2	1	1	2	3	1004
1	1	1	3	2	1	1	1	3	1	1	1	3	1	1	3	2	2	2	3	1	1	1	3	1005
2	2	2	1	3	2	2	3	1	1	3	1	1	2	1	3	1	1	1	3	1	1	1	3	1006
3	2	3	2	1	1	2	1	1	3	1	3	2	3	1	1	2	1	3	2	1	1	2	2	1007
2	1	2	2	3	1	1	1	2	1	1	3	1	3	1	3	1	2	2	2	3	2	3	1	1008
1	2	3	1	3	1	1	1	3	1	1	3	1	1	3	2	2	1	1	3	1	2	2	2	1009
1	1	3	1	3	2	3	1	3	2	1	2	1	2	2	3	2	2	1	1	1	3	1	1	1010
2	2	2	3	2	1	1	1	3	2	3	1	2	3	1	2	3	2	1	1	3	1	2	1	1011
3	1	2	3	2	2	1	2	3	2	3	1	2	3	1	1	1	2	1	2	3	2	1	2	1012
3	2	1	3	1	1	2	1	1	1	3	2	3	2	2	1	1	1	3	2	3	2	2	1	1013
1	1	1	3	1	3	2	1	2	3	2	3	2	3	2	1	2	3	1	2	1	2	2	2	1014
1	1	1	3	1	2	1	1	3	1	3	2	2	1	3	2	1	1	1	2	2	3	2	3	1015
1	1	3	1	1	2	2	1	3	1	3	1	1	2	1	1	3	2	3	2	3	1	2	1	1016
3	1	2	1	1	3	1	1	1	3	2	3	1	1	1	2	3	2	1	1	1	2	2	3	1017
3	1	2	3	1	1	1	3	1	2	3	2	2	2	1	1	1	3	2	2	2	3	2	2	1018
1	3	2	3	2	1	1	3	2	1	1	2	1	1	3	2	2	2	3	1	3	1	1	1	1019
3	2	2	3	1	3	1	1	2	2	1	3	1	1	2	2	2	3	1	2	1	1	1	3	1020
2	2	1	1	3	1	1	1	2	2	2	3	2	1	2	3	2	3	2	2	3	2	2	3	1021
1	3	1	1	3	1	2	2	2	1	3	1	2	3	1	1	1	2	3	1	3	2	2	2	1022
2	1	1	3	2	2	3	1	3	1	2	1	1	1	3	1	2	3	1	2	1	2	2	3	1023
2	3	1	3	1	2	1	3	2	2	2	3	2	1	1	2	1	2	3	2	2	2	3	2	1024

Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern																							Sequence Identifier		
1	3	2	2	2	3	1	1	1	2	2	3	2	1	1	3	2	2	2	3	1	2	3	1	1025	
2	1	3	1	1	2	2	3	1	2	2	1	1	2	3	1	2	3	1	3	2	1	3	2	1026	
1	3	1	3	1	2	2	2	3	2	1	1	2	1	1	3	2	1	2	2	3	1	1	3	1027	
1	2	1	1	2	3	1	2	3	2	1	1	2	3	2	1	1	3	2	1	3	2	3	2	1028	
2	3	1	1	1	2	2	2	3	1	2	3	1	3	1	3	1	2	1	2	3	2	2	1	1029	
2	3	2	3	2	1	1	1	3	2	1	2	1	3	2	2	2	1	2	3	2	2	1	3	1030	
2	3	1	1	2	1	1	3	2	3	1	1	1	2	1	3	1	1	2	3	1	1	2	3	1031	
1	1	1	3	1	1	1	3	1	2	2	3	2	1	1	2	1	1	3	2	1	3	1	3	1032	
1	1	2	3	1	1	1	2	1	3	2	3	2	2	1	1	1	2	3	1	3	2	3	2	1033	
3	2	1	3	1	2	1	1	1	3	1	2	3	2	3	1	1	2	2	1	2	3	1	2	1034	
3	1	2	1	3	2	1	2	1	2	3	2	3	2	3	2	1	2	2	2	3	2	2	2	1035	
1	2	3	2	2	2	3	2	1	3	1	1	1	2	3	2	2	2	3	1	1	3	1	2	1036	
1	1	1	2	2	2	3	2	1	3	1	3	1	3	1	1	1	2	2	2	3	2	2	3	1037	
2	1	3	1	1	2	1	1	3	1	2	2	1	3	2	1	1	3	2	3	2	1	3	1	1038	
2	3	1	2	2	2	1	3	1	3	1	1	1	2	1	2	3	1	3	2	1	3	1	1	1039	
1	1	2	1	3	1	3	2	1	2	3	2	2	3	2	2	2	1	2	3	1	3	1	1	1040	
3	1	2	3	1	2	3	1	1	3	1	3	2	2	2	1	2	2	3	2	1	1	1	2	1041	
1	1	3	2	1	1	1	3	1	1	3	1	1	3	1	1	1	2	3	2	3	2	2	1	1042	
2	2	3	1	1	3	1	1	2	2	1	1	3	2	3	2	2	2	2	1	3	2	3	2	1	1043
1	3	1	1	1	3	1	1	2	3	2	2	3	1	2	2	2	1	2	3	1	2	3	2	1044	
3	1	2	2	1	1	1	3	1	3	1	2	3	2	2	3	1	2	2	3	1	1	1	2	1045	
1	1	2	3	1	2	1	1	2	2	3	2	2	3	1	3	1	3	1	3	2	1	1	2	1046	
3	2	2	2	3	2	2	3	1	1	1	3	2	3	2	1	1	1	3	2	1	2	1	2	1047	
2	3	1	3	2	2	1	2	1	2	3	1	3	1	1	1	3	2	3	2	1	1	2	2	1048	
2	2	3	2	3	1	3	1	1	1	3	1	1	3	2	1	2	1	2	1	3	1	1	2	1049	
3	2	1	1	3	2	2	2	1	3	1	3	2	2	1	2	1	3	1	3	2	2	2	1	1050	
3	1	2	1	3	1	2	1	3	1	2	1	1	3	2	2	1	1	2	2	3	1	1	3	1051	
1	3	1	3	1	2	3	1	2	2	3	2	2	2	1	2	3	2	1	2	2	1	2	3	1052	
1	1	1	3	2	2	1	1	3	1	1	1	2	2	3	2	1	3	2	3	1	2	1	3	1053	
2	2	2	3	1	2	1	2	2	3	2	2	2	3	2	3	1	3	2	3	2	1	2	1	1054	
1	2	2	2	3	2	1	3	1	1	1	3	2	2	3	2	2	1	2	3	1	3	2	2	1055	
3	1	2	2	2	3	1	3	2	1	1	3	2	2	2	1	2	1	3	1	2	3	1	1	1056	
1	1	3	1	2	1	1	1	3	2	3	1	3	2	3	1	2	2	2	1	3	1	2	1	1057	
3	1	2	1	2	2	3	2	1	1	3	1	2	1	2	3	2	2	3	2	1	1	1	3	1058	
3	2	1	1	3	1	3	2	3	2	1	2	2	3	2	1	1	3	2	2	1	1	2	2	1059	
3	2	3	2	3	1	2	2	1	3	2	1	1	2	3	1	1	3	2	1	2	2	2	1	1060	
3	2	1	1	3	1	1	1	3	1	2	2	1	1	3	2	3	2	2	1	3	2	1	1	1061	
1	3	2	1	3	1	1	1	3	2	2	3	1	1	1	2	2	3	1	2	2	1	2	3	1062	
2	1	1	3	1	3	1	1	3	2	2	3	1	3	2	1	1	2	3	2	1	2	2	2	1063	
3	2	2	1	1	3	1	1	1	2	1	3	2	1	3	1	2	1	1	3	2	3	1	1	1064	
2	1	1	3	2	1	1	1	2	2	3	1	1	1	3	2	3	2	1	2	1	3	2	3	1065	
1	1	3	1	2	3	2	1	2	3	2	2	2	1	2	2	3	2	2	3	2	3	2	1	1066	
1	2	2	2	1	3	1	1	2	1	2	1	3	2	3	1	1	3	1	3	1	2	1	3	1067	
3	2	2	1	2	3	1	1	1	3	1	3	2	1	2	3	2	3	2	2	1	1	1	2	1068	
2	1	2	2	1	2	3	2	3	1	1	3	1	1	3	1	1	2	3	1	2	2	1	3	1069	
2	1	1	2	1	1	3	2	2	3	1	1	3	1	3	1	1	2	2	3	2	2	3	2	1070	
2	3	1	2	3	2	2	2	3	1	2	3	2	1	1	2	2	3	2	2	1	1	1	3	1071	
3	2	3	1	1	1	3	1	2	2	2	3	1	3	2	2	2	3	2	1	2	1	1	2	1072	
1	3	1	3	1	1	2	1	2	1	3	1	2	2	3	1	3	1	2	2	2	3	2	2	1073	
2	2	2	3	1	3	1	2	3	2	3	1	2	3	1	2	1	1	1	3	2	2	1	1	1074	
3	2	2	3	2	1	1	1	2	2	3	2	1	3	2	1	1	1	3	1	1	3	2	1	1075	
3	2	3	2	2	1	2	3	1	2	3	2	2	3	2	2	2	2	3	2	1	2	2	1	2	1076
1	2	2	1	2	2	3	2	3	2	1	3	1	2	2	3	2	1	2	2	1	1	3	1	3	1077
3	2	2	1	3	1	1	1	3	1	2	2	2	1	3	1	1	3	2	2	1	3	2	2	1078	
2	2	3	2	3	2	1	2	2	1	1	3	1	3	1	3	2	3	1	1	1	2	1	2	1079	
3	2	2	2	1	1	3	1	2	1	3	1	1	1	3	1	3	2	3	1	2	2	2	1	1080	



Table IA: Numeric sequences corresponding to nucleotide base patterns of a set of oligonucleotides

Numeric Pattern																							Sequence Identifier	
3	1	2	3	2	1	2	1	1	1	3	1	3	2	1	2	3	2	2	1	2	1	1	3	1137
1	3	2	3	1	3	1	2	2	2	1	3	1	1	3	1	2	3	2	2	1	2	2	1	1138
1	2	3	1	3	1	1	2	2	2	3	2	2	1	1	1	3	1	3	1	1	1	3	2	1139
1	1	1	3	1	1	2	2	1	3	2	1	2	3	1	2	1	3	1	2	3	1	3	1	1140
2	1	3	1	3	2	2	3	2	1	2	1	3	2	2	2	1	2	1	3	2	2	3	1	1141
3	2	1	3	1	1	2	3	1	2	2	3	2	2	2	1	3	1	1	3	1	2	2	2	1142
3	2	2	2	1	2	3	2	2	2	3	1	3	1	1	3	1	3	2	2	1	2	2	2	1143
2	1	3	1	1	3	2	2	2	3	1	1	1	3	2	2	1	2	2	3	1	2	2	3	1144
3	1	2	3	1	1	3	1	3	2	1	2	2	2	3	2	2	1	2	1	2	3	2	1	1145
3	1	2	3	1	1	2	1	2	1	3	2	1	1	3	2	1	2	2	3	1	3	2	1	1146
2	1	3	2	3	1	2	3	1	1	1	2	2	2	3	1	3	1	2	1	3	1	2	1	1147
3	1	1	1	3	1	1	1	2	2	3	1	1	3	1	3	2	2	2	3	1	2	1	2	1148
1	2	2	2	3	1	3	2	1	2	2	2	3	2	3	2	1	2	2	3	1	1	2	3	1149
1	2	3	1	3	2	2	3	1	1	1	2	2	2	3	1	1	3	2	1	2	2	3	2	1150
2	2	1	1	2	1	3	2	3	1	3	1	3	1	3	2	1	2	1	2	3	2	1	1	1151
1	2	2	1	1	3	1	3	1	3	2	3	1	3	2	1	1	1	2	3	2	1	1	1	1152
1	1	3	1	1	2	1	3	1	2	3	1	3	1	2	2	1	3	1	1	1	2	1	3	1153
1	3	2	2	2	1	1	1	3	1	3	2	2	1	3	1	1	2	2	3	1	1	1	3	1154
3	2	1	1	3	1	2	2	2	3	2	2	3	1	1	2	1	1	1	3	1	1	3	1	1155
1	3	1	3	1	1	1	3	1	1	3	2	2	1	1	1	3	2	3	1	2	1	2	2	1156
2	1	1	2	1	3	1	3	1	1	3	1	3	1	3	1	2	3	2	1	2	3	1	1	1157
2	2	1	2	2	1	3	2	3	1	2	1	1	3	2	3	1	1	3	2	2	2	1	3	1158
1	2	1	1	2	3	2	1	1	1	3	1	2	3	1	3	2	2	2	1	2	3	1	3	1159
2	2	3	1	2	2	2	3	1	3	1	3	2	2	3	1	2	1	1	3	1	2	2	2	1160
1	2	3	1	2	2	1	2	2	3	2	3	2	3	2	1	3	1	1	2	2	1	3	1	1161
2	1	2	1	1	1	3	1	2	1	2	1	3	2	1	3	1	2	3	1	2	3	2	3	1162
2	2	2	1	3	2	2	3	1	3	1	2	3	1	1	3	2	2	1	2	2	1	3	1	1163
1	2	2	3	1	1	2	2	3	1	2	1	2	1	3	2	3	2	1	1	1	3	2	3	1164
3	1	1	3	1	1	1	3	1	2	2	1	2	2	3	2	1	2	2	3	1	3	2	2	1165
1	2	2	3	1	3	2	3	2	1	3	2	3	1	2	2	1	3	1	1	1	2	1	1	1166
1	1	2	1	1	1	3	2	3	2	2	2	1	1	3	1	3	2	1	3	1	3	2	1	1167
3	2	1	3	1	3	1	2	1	1	2	2	3	1	2	3	2	3	2	1	1	2	2	2	1168

In Table IA, each of the numerals 1 to 3 (numeric identifiers) represents a nucleotide base and the pattern of numerals 1 to 3 of the sequences in the above list corresponds to the pattern of nucleotide bases present in the oligonucleotides of Table I, which oligonucleotides have been found to be non-cross-hybridizing, as described further in the detailed examples. Each nucleotide base is selected from the group of nucleotide bases consisting of A, C, G, and T/U. A particularly preferred embodiment of the invention, in which a specific base is assigned to each numeric identifier is shown in Table I, below.

In one broad aspect, the invention is a composition comprising molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on a group of sequences as specified by numeric identifiers set out in Table IA. In the sequences, each of 1 to 3 is a nucleotide base

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selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base provided that:

for any pair of sequences of the set:

$M1 \leq 15$ ,  $M2 \leq 12$ ,  $M3 \leq 19$ ,  $M4 \leq 15$ , and  $M5 \leq 18$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of maximum score;

wherein:

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):

(i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,

(ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,

(iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and

(iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

5 An explanation of the meaning of the parameters set out above is given in the section describing detailed embodiments.

In another broad aspect, the invention is a composition containing molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on a group of sequences as set out in Table IA wherein each of 1 to 3 is a nucleotide base selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base provided that:

for any pair of sequences of the set:



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$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of maximum score; wherein

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):

(i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,

(ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,

(iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and

(iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

In another broad aspect, the invention is a composition comprising molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on a group of sequences set out in Table IA wherein each of 1 to 3 is a nucleotide base selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base provided that:

for any pair of sequences of the set:

$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum

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score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of maximum score, wherein:

the score of an alignment is determined according to the equation  $3A - B - 3C - D$ , wherein:

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

In preferred aspects, the invention provides a composition in which, for the group of 24mer sequences in which 1 = A, 2 = T and 3 = G, under a defined set of conditions in which the maximum degree of hybridization between a sequence and any complement of a different

5 sequence of the group of 24mer sequences does not exceed 30% of the degree of hybridization between said sequence and its complement, for all said oligonucleotides of the composition, the maximum degree of hybridization between an oligonucleotide and a complement of any other oligonucleotide of the composition does not exceed 50% of the degree of  
10 hybridization of the oligonucleotide and its complement.

More preferably, the maximum degree of hybridization between a sequence and any complement of a different sequence does not exceed 30% of the degree of hybridization between said sequence and its complement, the degree of hybridization between each sequence and its complement  
15 varies by a factor of between 1 and up to 10, more preferably between 1 and up to 9, more preferably between 1 and up to 8, more preferably between 1 and up to 7, more preferably between 1 and up to 6, and more preferably between 1 and up to 5.

It is also preferred that the maximum degree of hybridization  
20 between a sequence and any complement of a different sequence does not exceed 25%, more preferably does not exceed 20%, more preferably does not exceed 15%, more preferably does not exceed 10%, more preferably does not exceed 5%.

Even more preferably, the above-referenced defined set of  
25 conditions results in a level of hybridization that is the same as the

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level of hybridization obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C.

In the composition, the defined set of conditions can include the group of 24mer sequences being covalently linked to beads.

5 In a particular preferred aspect, for the group of 24mers the maximum degree of hybridization between a sequence and any complement of a different sequence does not exceed 15% of the degree of hybridization between said sequence and its complement and the degree of hybridization between each sequence and its complement varies by a factor of between 1  
10 and up to 9, and for all oligonucleotides of the set, the maximum degree of hybridization between an oligonucleotide and a complement of any other oligonucleotide of the set does not exceed 20% of the degree of hybridization of the oligonucleotide and its complement.

It is possible that each 1 is one of A, T/U, G and C; each 2 is  
15 one of A, T/U, G and C; and each 3 is one of A, T/U, G and C; and each of 1, 2 and 3 is selected so as to be different from all of the others of 1, 2 and 3. More preferably, 1 is A or T/U, 2 is A or T/U and 3 is G or C. Even more preferably, 1 is A, 2 is T/U, and 3 is G.

In certain preferred composition, each of the oligonucleotides is  
20 from twenty-two to twenty-six bases in length, or from twenty-three to twenty-five, and preferably, each oligonucleotide is of the same length as every other said oligonucleotide.

In a particularly preferred embodiment, each oligonucleotide is twenty-four bases in length.

25 It is preferred that no oligonucleotide contains more than four contiguous bases that are identical to each other.

It is also preferred that the number of G's in each oligonucleotide does not exceed  $L/4$  where L is the number of bases in said sequence.

30 For reasons described below, the number of G's in each said oligonucleotide is preferred not to vary from the average number of G's in all of the oligonucleotides by more than one. Even more preferably, the number of G's in each said oligonucleotide is the same as every other said oligonucleotide. In the embodiment disclosed below in which  
35 oligonucleotides were tested, the sequence of each was twenty-four bases in length and each oligonucleotide contained 6 G's.

It is also preferred that, for each nucleotide, there is at most six bases other than G between every pair of neighboring pairs of G's.

Also, it is preferred that, at the 5'-end of each oligonucleotide  
40 at least one of the first, second, third, fourth, fifth, sixth and

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seventh bases of the sequence of the oligonucleotide is a G. Similarly, it is preferred, at the 3'-end of each oligonucleotide that at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence of the oligonucleotide is a G.

5 It is possible to have sequence compositions that include one hundred and sixty said molecules, or that include one hundred and seventy said molecules, or that include one hundred and eighty said molecules, or that include one hundred and ninety said molecules, or that include two hundred said molecules, or that include two hundred and  
10 twenty said molecules, or that include two hundred and forty said molecules, or that include two hundred and sixty said molecules, or that include two hundred and eighty said molecules, or that include three hundred said molecules, or that include four hundred said molecules, or that include five hundred said molecules, or that include six hundred  
15 said molecules, or that include seven hundred said molecules, or that include eight hundred said molecules, or that include nine hundred said molecules, or that include one thousand said molecules.

It is possible, in certain applications, for each molecule to be linked to a solid phase support so as to be distinguishable from a  
20 mixture containing other of the molecules by hybridization to its complement. Such a molecule can be linked to a defined location on a solid phase support such that the defined location for each molecule is different than the defined location for different others of the molecules.

25 In certain embodiments, each solid phase support is a microparticle and each said molecule is covalently linked to a different microparticle than each other different said molecule.

In another broad aspect, the invention is a composition comprising a set of 150 molecules for use as tags or tag complements wherein each  
30 molecule includes an oligonucleotide having a sequence of at least sixteen nucleotide bases wherein for any pair of sequences of the set:

$M1 > 19/24 \times L1$ ,  $M2 > 17/24 \times L1$ ,  $M3 > 21/24 \times L1$ ,  $M4 > 18/24 \times L1$ ,  $M5 > 20/24 \times L1$ , where  $L1$  is the length of the shortest sequence of the pair, where:

$M1$  is the maximum number of matches for any alignment of the pair of sequences in which there are no internal indels;

$M2$  is the maximum length of a block of matches for any alignment of the pair of sequences;

$M3$  is the maximum number of matches for any alignment of the pair of sequences having a maximum score;

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M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of the pair of sequences of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of the pair of sequences of maximum score, wherein:

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):

(i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,

(ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,

(iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and

(iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

In yet another broad aspect, the invention is a composition that includes a set of 150 molecules for use as tags or tag complements wherein each molecule has an oligonucleotide having a sequence of at least sixteen nucleotide bases wherein for any pair of sequences of the

5 set:

$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment of the pair of sequences in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment of the pair of sequences;

M3 is the maximum number of matches for any alignment of the pair of sequences having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of the pair of sequences of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of the pair of sequences of maximum score, wherein:

the score of a said alignment is determined according to the equation

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3A - B - 3C - D, wherein:

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment.

In certain embodiments of the invention, each sequence of a composition has up to fifty bases. More preferably, however, each sequence is between sixteen and forty bases in length, or between sixteen and thirty-five bases in length, or between eighteen and thirty  
5 bases in length, or between twenty and twenty-eight bases in length, or between twenty-one and twenty-seven bases in length, or between twenty-two and twenty-six bases in length.

Often, each sequence is of the same length as every other said sequence. In particular embodiments disclosed herein, each sequence is  
10 twenty-four bases in length.

Again, it can be preferred that no sequence contains more than four contiguous bases that are identical to each other, etc., as described above.

In certain preferred embodiments, the composition is such that,  
15 under a defined set of conditions, the maximum degree of hybridization between an oligonucleotide and any complement of a different oligonucleotide of the composition does not exceed about 30% of the degree of hybridization between said oligonucleotide and its complement, more preferably 20%, more preferably 15%, more preferably 10%, more  
20 preferably 6%.

Preferably, the set of conditions results in a level of hybridization that is the same as the level of hybridization obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C, and the oligonucleotides are covalently  
25 linked to microparticles. Of course it is possible that these specific conditions be used for determining the level of hybridization.

It is also preferred that under such a defined set of conditions, the degree of hybridization between each oligonucleotide and its complement varies by a factor of between 1 and up to 8, more preferably  
30 up to 7, more preferably up to 6, more preferably up to 5. In a particular disclosed embodiment, the observed variance in the degree of hybridization was a factor of only 5.3, i.e., the degree of

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hybridization between each oligonucleotide and its complement varied by a factor of between 1 and 5.6.

In certain preferred embodiments, under the defined set of conditions, the maximum degree of hybridization between a said  
5 oligonucleotide and any complement of a different oligonucleotide of the composition does not exceed about 15%, more preferably 10%, more preferably 6%.

In one preferred embodiment, the set of conditions results in a level of hybridization that is the same as the level of hybridization  
10 obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C, and the oligonucleotides are covalently linked to microparticles.

Also, under the defined set of conditions, it is preferred that the degree of hybridization between each oligonucleotide and its  
15 complement varies by a factor of between 1 and up to 8, more preferably up to 7, more preferably up to 6, more preferably up to 5.

Any composition of the invention can include one hundred and sixty of the oligonucleotide molecules, or one hundred and seventy of the oligonucleotide molecules, or one hundred and eighty of the oligonucleotide molecules, or one hundred and ninety of the oligonucleotide molecules, or two hundred of the oligonucleotide molecules, or two hundred and twenty of the oligonucleotide molecules, or two hundred and forty of the oligonucleotide molecules, or two hundred and sixty of the oligonucleotide molecules, or two hundred and  
25 eighty of the oligonucleotide molecules, or three hundred of the oligonucleotide molecules, or four hundred of the oligonucleotide molecules, or five hundred of the oligonucleotide molecules, or six hundred of the oligonucleotide molecules, or seven hundred of the oligonucleotide molecules, or eight hundred of the oligonucleotide molecules, or nine hundred of the oligonucleotide molecules, or one thousand or more of the oligonucleotide molecules.

A composition of the invention can be a family of tags, or it can be a family of tag complements.

An oligonucleotide molecule belonging to a family of molecules of  
35 the invention can have incorporated therein one more analogues of nucleotide bases, preference being given those that undergo normal Watson-Crick base pairing.

The invention includes kits for sorting and identifying polynucleotides. Such a kit can include one or more solid phase  
40 supports each having one or more spatially discrete regions, each such

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region having a uniform population of substantially identical tag complements covalently attached. The tag complements are made up of a set of oligonucleotides of the invention.

5 The one or more solid phase supports can be a planar substrate in which the one or more spatially discrete regions is a plurality of spatially addressable regions.

The tag complements can also be coupled to microparticles. Microparticles preferably each have a diameter in the range of from 5 to 40  $\mu\text{m}$ .

10 Such a kit preferably includes microparticles that are spectrophotometrically unique, and therefore distinguishable from each other according to conventional laboratory techniques. Of course for such kits to work, each type of microparticle would generally have only one tag complement associated with it, and usually there would be a  
15 different oligonucleotide tag complement associated with (attached to) each type of microparticle.

The invention includes methods of using families of oligonucleotides of the invention.

20 One such method is of analyzing a biological sample containing a biological sequence for the presence of a mutation or polymorphism at a locus of the nucleic acid. The method includes:

- (A) amplifying the nucleic acid molecule in the presence of a first primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements of the invention to form an amplified molecule with a 5'-end with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecule in the presence of a polymerase and a second primer having 5'-end complementary the 3'-end of the amplified sequence, with the 3'-end of the second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is: (i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus of the amplified sequence;
- (C) specifically hybridizing the second primer to a tag complement having the tag complement sequence of (A); and
- (D) detecting the nucleotide derivative incorporated into the second primer in (B) so as to identify the base located at the locus of the nucleic



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acid.

In another method of the invention, a biological sample containing a plurality of nucleic acid molecules is analyzed for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for each nucleic acid molecule. This method includes steps of:

- (A) amplifying the nucleic acid molecule in the presence of a first primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements of the invention to form an amplified molecule with a 5'-end with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecule in the presence of a polymerase and a second primer having 5'-end complementary the 3'-end of the amplified sequence, the 3'-end of the second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is: (i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus of the amplified molecule;
- (C) specifically hybridizing the second primer to a tag complement having the tag complement sequence of (A); and
- (D) detecting the nucleotide derivative incorporated into the second primer in (B) so as to identify the base located at the locus of the nucleic acid;

wherein each tag of (A) is unique for each nucleic acid molecule and steps (A) and (B) are carried out with said nucleic molecules in the presence of each other.

5 Another method includes analyzing a biological sample that contains a plurality of double stranded complementary nucleic acid molecules for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for each nucleic acid molecule. The method includes steps of:

- (A) amplifying the double stranded molecule in the presence of a pair of first primers, each primer having an identical 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements of the invention to form amplified molecules with 5'-ends with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecules in the presence of a polymerase and a

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pair of second primers each second primer having a 5'-end complementary a 3'-end of the amplified sequence, the 3'-end of each said second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is:

(i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other;

(C) specifically hybridizing each of the second primers to a tag complement having the tag complement sequence of (A); and

(D) detecting the nucleotide derivative incorporated into the second primers in (B) so as to identify the base located at said locus;

wherein the sequence of each tag of (A) is unique for each nucleic acid molecule and steps (A) and (B) are carried out with said nucleic molecules in the presence of each other.

In yet another aspect, the invention is a method of analyzing a biological sample containing a plurality of nucleic acid molecules for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for each nucleic acid molecule, the method including

5 steps of:

(a) hybridizing the molecule and a primer, the primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements of the invention and a 3'-end extending to immediately adjacent the locus;

(b) enzymatically extending the 3'-end of the primer in the presence of a plurality of nucleoside triphosphate derivatives each of which is: (i) capable of enzymatic incorporation onto the 3'-end of a growing nucleotide strand; (ii) causes termination of said extension; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus;

(c) specifically hybridizing the extended primer formed in step (b) to a tag complement having the tag complement sequence of (a); and

(d) detecting the nucleotide derivative incorporated into the primer in step (b) so as to identify the base located at the locus of the nucleic acid molecule;

wherein each tag of (a) is unique for each nucleic acid molecule and steps (a) and (b) are carried out with said nucleic molecules in the presence of each other.

The derivative can be a dideoxy nucleoside triphosphate.

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Each respective complement can be attached as a uniform population of substantially identical complements in spacially discrete regions on one or more solid phase support(s).

Each tag complement can include a label, each such label being  
5 different for respective complements, and step (d) can include detecting the presence of the different labels for respective hybridization complexes of bound tags and tag complements.

Another aspect of the invention includes a method of determining the presence of a target suspected of being contained in a mixture. The  
10 method includes the steps of:

- (i) labelling the target with a first label;
- (ii) providing a first detection moiety capable of specific binding to the target and including a first tag;
- (iii) exposing a sample of the mixture to the detection moiety under conditions suitable to permit (or cause) said specific binding of the molecule and target;
- (iv) providing a family of suitable tag complements of the invention wherein the family contains a first tag complement having a sequence complementary to that of the first tag;
- (v) exposing the sample to the family of tag complements under conditions suitable to permit (or cause) specific hybridization of the first tag and its tag complement;
- (vi) determining whether a said first detection moiety hybridized to a first said tag complement is bound to a said labelled target in order to determine the presence or absence of said target in the mixture.

Preferably, the first tag complement is linked to a solid support at a specific location of the support and step (vi) includes detecting the presence of the first label at said specified location.

Also, the first tag complement can include a second label and step  
15 (vi) includes detecting the presence of the first and second labels in a hybridized complex of the moiety and the first tag complement.

Further, the target can be selected from the group consisting of organic molecules, antigens, proteins, polypeptides, antibodies and nucleic acids. The target can be an antigen and the first molecule can  
20 be an antibody specific for that antigen.

The antigen is usually a polypeptide or protein and the labelling step can include conjugation of fluorescent molecules, digoxigenin, biotinylation and the like.

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The target can be a nucleic acid and the labelling step can include incorporation of fluorescent molecules, radiolabelled nucleotide, digoxigenin, biotinylation and the like.

## 5 DETAILED DESCRIPTION OF THE INVENTION

### FIGURES

Reference is made to the attached figures in which,

Figure 1 illustrates generally the steps followed to obtain a family of sequences of the present invention;

10 Figure 2 shows the intensity of the signal (MFI) for each perfectly matched sequence (probe sequences indicated in Table I) and its complement (target, at 50 fmol) obtained as described in Example 1;

Figure 3 is a three dimensional representation showing cross-hybridization observed for the sequences of Figure 2 as described in  
15 Example 1. The results shown in Figure 2 are reproduced along the diagonal of the drawing; and

Figure 4 is illustrative of results obtained for an individual target (SEQ ID NO:90, target No. 90) when exposed to the 100 probes of Example 1. The MFI for each bead is plotted.

### 20 DETAILED EMBODIMENTS

The invention provides a method for sorting complex mixtures of molecules by the use of families of oligonucleotide sequence tags. The families of oligonucleotide sequence tags are designed so as to provide  
25 minimal cross hybridization during the sorting process. Thus any sequence within a family of sequences will not significantly cross-hybridize with any other sequence derived from that family under appropriate hybridization conditions known by those skilled in the art. The invention is particularly useful in highly parallel processing of analytes.

#### 30 Families of Oligonucleotide Sequence Tags

The present invention includes a family of 24mer polynucleotides that have been demonstrated to be minimally cross-hybridizing with each other. This family of polynucleotides is thus useful as a family of tags, and their  
35 complements as tag complements.

In order to be considered for inclusion into the family, a sequence had to satisfy a certain number of rules regarding its composition. For example, repetitive regions that present potential hybridization problems such as four or more of a similar base (e.g., AAAA or TTTT) or pairs of Gs were forbidden.

40 Another rule is that each sequence contains exactly six Gs and no Cs, in order

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to have sequences that are more or less isothermal. Also required for a 24mer to be included is that there must be at most six bases between every neighboring pair of Gs. Another way of putting this is that there are at most six non-Gs between any two consecutive Gs. Also, each G nearest the 5'-end (resp. 3'-end) of its oligonucleotide (the left-hand (resp. right-hand) side as written in Table I) was required to occupy one of the first to seventh positions (counting the 5'-terminal (resp. 3'-terminal) position as the first position.)

The process used to design families of sequences that do not exhibit cross-hybridization behavior is illustrated generally in Figure 1). Depending on the application for which these families of sequences will be used, various rules are designed. A certain number of rules can specify constraints for sequence composition (such as the ones described in the previous paragraph). The other rules are used to judge whether two sequences are too similar. Based on these rules, a computer program can derive families of sequences that exhibit minimal or no cross-hybridization behavior. The exact method used by the computer program is not crucial since various computer programs can derive similar families based on these rules. Such a program is for example described in international patent application No. PCT/CA 01/00141 published under WO 01/59151 on August 16, 2001. Other programs can use different methods, such as the ones summarized below.

A first method of generating a maximum number of minimally cross-hybridizing polynucleotide sequences starts with any number of non-cross-hybridizing sequences, for example just one sequence, and increases the family as follows. A certain number of sequences is generated and compared to the sequences already in the family. The generated sequences that exhibit too much similarity with sequences already in the family are dropped. Among the "candidate sequences" that remain, one sequence is selected and added to the family. The other candidate sequences are then compared to the selected sequence, and the ones that show too much similarity are dropped. A new sequence is selected from the remaining candidate sequences, if any, and added to the family, and so on until there are no candidate sequences left. At this stage, the process can be repeated (generating a certain number of sequences and comparing them to the sequences in the family, etc.) as often as desired. The family obtained at the end of this method contains only minimally cross-hybridizing sequences.

A second method of generating a maximum number of minimally cross-hybridizing polynucleotide sequences starts with a fixed-size family of polynucleotide sequences. The sequences of this family can be generated randomly or designed by some other method. Many sequences in this family may

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not be compatible with each other, because they show too much similarity and are not minimally cross-hybridizing. Therefore, some sequences need to be replaced by new ones, with less similarity. One way to achieve this consists of repeatedly replacing a sequence of the family by the best (that is, lowest  
5 similarity) sequence among a certain number of (for example, randomly generated) sequences that are not part of the family. This process can be repeated until the family of sequences shows minimal similarity, hence minimal cross-hybridizing, or until a set number of replacements has occurred. If, at the end of the process, some sequences do not obey the similarity rules that  
10 have been set, they can be taken out of the family, thus providing a somewhat smaller family that only contains minimally cross-hybridizing sequences. Some additional rules can be added to this method in order to make it more efficient, such as rules to determine which sequence will be replaced.

Such methods have been used to obtain the 1168 non-cross-hybridizing  
15 tags of Table I that are the subject of this patent application.

One embodiment of the invention is a composition comprising molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on the group of sequences set out in Table IA, wherein each of the  
20 numeric identifiers 1 to 3 (see the Table) is a nucleotide base selected to be different from the others of 1 to 3. According to this embodiment, several different families of specific sets of oligonucleotide sequences are described, depending upon the assignment of bases made to the numeric identifiers 1 to 3.

25 The sequences contained in Table I have a mathematical relationship to each other, described as follows.

Let  $S$  and  $T$  be two DNA sequences of lengths  $s$  and  $t$  respectively. While the term "alignment" of nucleotide sequences is widely used in the field of biotechnology, in the context of this invention the term has a  
30 specific meaning illustrated here. An alignment of  $S$  and  $T$  is a  $2 \times p$  matrix  $A$  (with  $p \geq s$  and  $p \geq t$ ) such that the first (or second) row of  $A$  contains the characters of  $S$  (or  $T$  respectively) in order, interspersed with  $p-s$  (or  $p-t$  respectively) spaces. It is assumed that no column of the alignment matrix contains two spaces, i.e., that any alignment in which  
35 a column contains two spaces is ignored and not considered here. The columns containing the same base in both rows are called *matches*, while the columns containing different bases are called *mismatches*. Each column of an alignment containing a space in its first row is called an *insertion* and each column containing a space in its second row is called  
40 a *deletion* while a column of the alignment containing a space in either

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row is called an *indel*. Insertions and deletions within a sequence are represented by the character '-'. A *gap* is a continuous sequence of spaces in one of the rows (that is neither immediately preceded nor immediately followed by another space in the same row), and the *length* of a *gap* is the number of spaces in that gap. An *internal gap* is one in which its first space is preceded by a base and its last space is followed by a base and an *internal indel* is an indel belonging to an internal gap. Finally, a *block* is a continuous sequence of matches (that is neither immediately preceded nor immediately followed by another match), and the *length* of a *block* is the number of matches in that block. In order to illustrate these definitions, two sequences  $S =$  TGATCGTAGCTACGCCGCG (of length  $s = 19$ ; SEQ ID NO:1169) and  $T =$  CGTACGATTGCAACGT (of length  $t = 16$ ; SEQ ID NO:1170) are considered. Exemplary alignment  $R_1$  of  $S$  and  $T$  (with  $p = 23$ ) is:

Alignment  $R_1$ :

-	-	-	-	T	G	A	T	C	G	T	A	G	C	T	A	C	G	C	C	G	C	G
C	G	T	A	C	G	A	T	-	-	T	-	G	C	A	A	C	G	T	-	-	-	-

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23

Columns 1 to 4, 9, 10, 12 and 20 to 23 are indels, columns 6, 7, 8, 11, 13, 14, 16, 17 and 18 are matches, and columns 5, 15 and 19 are mismatches. Columns 9 and 10 form a gap of length 2, while columns 16 to 18 form a block of length 3. Columns 9, 10 and 12 are internal indels.

A score is assigned to the alignment  $A$  of two sequences by assigning weights to each of matches, mismatches and gaps as follows:

- the reward for a match  $m$ ,
- the penalty for a mismatch  $mm$ ,
- the penalty for opening a gap  $og$ ,
- the penalty for extending a gap  $eg$ .

Once these values are set, a score to each column of the alignment is assigned according to the following rules:

1. assign 0 to each column preceding the first match and to each column following the last match.
2. for each of the remaining columns, assign  $m$  if it is a match,  $-mm$  if it is a mismatch,  $-og-eg$  if it is the first indel

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of a gap, -eg if it is an indel but not the first indel of a gap.

The score of the alignment A is the sum of the scores of its columns. An alignment is said to be of maximum score if no other alignment of the same two sequences has a higher score (with the same values of *m*, *mm*, *og* and *eg*). A person knowledgeable in the field will recognize this method of scoring an alignment as scoring a local (as opposed to global) alignment with affine gap penalties (that is, gap penalties that can distinguish between the first indel of a gap and the other indels). It will be appreciated that the total number of indels that open a gap is the same as the total number of gaps and that an internal indel is not one of those assigned a 0 in rule (1) above. It will also be noted that foregoing rule (1) assigns a 0 for non-internal mismatches. An internal mismatch is a mismatch that is preceded and followed (not necessarily immediately) by a match.

As an illustration, if the values of *m*, *mm*, *og* and *eg* are set to 3, 1, 2 and 1 respectively, alignment R<sub>1</sub> has a score of 19, determined as shown below:

20

#### Scoring of Alignment R<sub>1</sub>

-	-	-	-	T	G	A	T	C	G	T	A	G	C	T	A	C	G	C	C	G	C	G
C	G	T	A	C	G	A	T	-	-	T	-	G	C	A	A	C	G	T	-	-	-	-

0 0 0 0 0 3 3 3 -3 -1 3 -3 3 3 -1 3 3 3 0 0 0 0 0

Note that for two given sequences S and T, there are numerous alignments. There are often several alignments of maximum score.

Based on these alignments, five sequence similarity measures are defined as follows. For two sequences S and T, and weights {*m*, *mm*, *og*, *eg*}:

- M1 is the maximum number of matches over all alignments free of internal indels;
- M2 is the maximum length of a block over all alignments;
- M3 is the maximum number of matches over all alignments of maximum score;
- M4 is the maximum sum of the lengths of the longest two blocks over all alignments of maximum score;



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- $M5$  is the maximum sum of the lengths of all the blocks of length at least 3, over all alignments of maximum score.

Notice that, by definition, the following inequalities between these similarity measures are obtained:  $M4 \leq M3$  and  $M5 \leq M3$ . Also, in order to determine  $M2$  it is sufficient to determine the maximum length of a block over all alignments free of internal indels. For two given sequences, the values of  $M3$  to  $M5$  can vary depending on the values of the weights  $\{m, mm, og, eg\}$ , but not  $M1$  and  $M2$ .

For weights  $\{3, 1, 2, 1\}$ , the illustrated alignment is not a maximum score alignment of the two example sequences. But for weights  $\{6, 6, 0, 6\}$  it is; hence this alignment shows that for these two example sequences, and weights  $\{6, 6, 0, 6\}$ ,  $M2 \geq 3$ ,  $M3 \geq 9$ ,  $M4 \geq 6$  and  $M5 \geq 6$ . In order to determine the exact values of  $M1$  to  $M5$ , all the necessary alignments need to be considered.  $M1$  and  $M2$  can be found by looking at the  $s+t-1$  alignments free of internal indels, where  $s$  and  $t$  are the lengths of the two sequences considered. Mathematical tools known as dynamic programming can be implemented on a computer and used to determine  $M3$  to  $M5$  in a very quick way. Using a computer program to do these calculations, it was determined that:

- with the weights  $\{6, 6, 0, 6\}$ ,  $M1 = 8$ ,  $M2 = 4$ ,  $M3 = 10$ ,  $M4 = 6$  and  $M5 = 6$ ;
- with the weights  $\{3, 1, 2, 1\}$ ,  $M1 = 8$ ,  $M2 = 4$ ,  $M3 = 10$ ,  $M4 = 6$  and  $M5 = 4$ .

According to the preferred embodiment of this invention, two sequences  $S$  and  $T$  each of length 24 are *too similar* if at least one of the following happens:

- $M1 > 16$  or
- $M2 > 13$  or
- $M3 > 20$  or
- $M4 > 16$  or
- $M5 > 19$

when using either weights  $\{6, 6, 0, 6\}$ , or  $\{6, 6, 5, 1\}$ , or  $\{6, 2, 5, 1\}$ , or  $\{6, 6, 6, 0\}$ . In other words, the five similarity measures between  $S$  and  $T$  are determined for each of the above four sets of weights, and checked against these thresholds (for a total of 20 tests).

The above thresholds of 16, 13, 20, 16 and 19, and the above sets of weights, were used to obtain the sequences listed in Table I. Additional sequences can thus be added to those of Table I as long as the above alignment rules are obeyed for all sequences.

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It is also possible to alter thresholds  $M1$ ,  $M2$ , etc., while remaining within the scope of this invention. It is thus possible to substitute or add sequences to those of Table I, or more generally to those of Table IA to obtain other sets of sequences that would also exhibit reasonably low cross-hybridization. More specifically, a set of 24mer sequences in which there are no two sequences that are too similar, where too similar is defined as:

- $M1 > 19$  or
- $M2 > 17$  or
- $M3 > 21$  or
- $M4 > 18$  or
- $M5 > 20$

when using either weights  $\{6, 6, 0, 6\}$ , or  $\{6, 6, 5, 1\}$ , or  $\{6, 2, 5, 1\}$ , or  $\{6, 6, 6, 0\}$ , would also exhibit low cross-hybridization.

Reducing any of the threshold values provides sets of sequences with even lower cross-hybridization. Alternatively, 'too similar' can also be defined as:

- $M1 > 19$  or
- $M2 > 17$  or
- $M3 > 21$  or
- $M4 > 18$  or
- $M5 > 20$

when using either weights  $\{3, 1, 2, 1\}$ . Alternatively, other combinations of weights will lead to sets of sequences with low cross-hybridization.

Notice that using weights  $\{6, 6, 0, 6\}$  is equivalent to using weights  $\{1, 1, 0, 1\}$ , or weights  $\{2, 2, 0, 2\}$ , ... (that is, for any two sequences, the values of  $M1$  to  $M5$  are exactly the same whether weights  $\{6, 6, 0, 6\}$  or  $\{1, 1, 0, 1\}$  or  $\{2, 2, 0, 2\}$  or any other multiple of  $\{1, 1, 0, 1\}$  is used).

When dealing with sequences of length other than 24, or sequences of various lengths, the definition of similarity can be adjusted. Such adjustments are obvious to the persons skilled in the art. For example, when comparing a sequence of length  $L1$  with a sequence of length  $L2$

(with  $L1 < L2$ ), they can be considered as too similar when

- $M1 > 19/24 \times L1$
- $M2 > 17/24 \times L1$
- $M3 > 21/24 \times L1$
- $M4 > 18/24 \times L1$

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M5 > 20/24 x L1

when using either weights {6, 6, 0, 6}, or {6, 6, 5, 1}, or {6, 2, 5, 1} or {6, 6, 6, 0}.

Polynucleotide sequences can be composed of a subset of natural bases most preferably A, T and G. Sequences that are deficient in one base possess useful characteristics, for example, in reducing potential secondary structure formation or reduced potential for cross hybridization with nucleic acids in nature. Also, it is preferable to have tag sequences that behave isothermally. This can be achieved for example by maintaining a constant base composition for all sequences such as six Gs and eighteen As or Ts for each sequence. Additional sets of sequences can be designed by extrapolating on the original family of non-cross-hybridizing sequences by simple methods known to those skilled in the art.

In order to validate the sequence set, a subset of sequences from the family of 1168 sequence tags was selected and characterized, in terms of the ability of these sequences to form specific duplex structures with their complementary sequences, and the potential for cross-hybridization within the sequence set. See Example 1, below. The subset of 100 sequences was randomly selected, and analyzed using the Luminex<sup>100</sup> LabMAP<sup>TM</sup> platform. The 100 sequences were chemically immobilized onto the set of 100 different Luminex microsphere populations, such that each specific sequence was coupled to one spectrally distinct microsphere population. The pool of 100 microsphere-immobilized probes was then hybridized with each of the 100 corresponding complementary sequences. Each sequence was examined individually for its specific hybridization with its complementary sequence, as well as for its non-specific hybridization with the other 99 sequences present in the reaction. This analysis demonstrated the propensity of each sequence to hybridize only to its complement (perfect match), and not to cross-hybridize appreciably with any of the other oligonucleotides present in the hybridization reaction.

It is within the capability of a person skilled in the art, given the family of sequences of Table I, to modify the sequences, or add other sequences while largely retaining the property of minimal cross-hybridization which the polynucleotides of Table I have been demonstrated to have.

There are 1168 polynucleotide sequences given in Table I. Since all 1168 of this family of polynucleotides can work with each other as a minimally cross-hybridizing set, then any plurality of polynucleotides that is a subset of the 1168 can also act as a minimally cross-hybridizing set of polynucleotides. An application in which, for example, 30 molecules are to be

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sorted using a family of polynucleotide tags and tag complements could thus use any group of 30 sequences shown in Table I. This is not to say that some subsets may be found in a practical sense to be more preferred than others. For example, it may be found that a particular subset is more tolerant of a wider variety of conditions under which hybridization is conducted before the degree of cross-hybridization becomes unacceptable.

It may be desirable to use polynucleotides that are shorter in length than the 24 bases of those in Table I. A family of subsequences (i.e., subframes of the sequences illustrated) based on those contained in Table I having as few as 10 bases per sequence could be chosen, so long as the subsequences are chosen to retain homological properties between any two of the sequences of the family important to their non cross-hybridization.

The selection of sequences using this approach would be amenable to a computerized process. Thus for example, a string of 10 contiguous bases of the first 24mer of Table I could be selected: AAATTGTGAAAGATTGTTGTGTA (SEQ ID NO:1).

The same string of contiguous bases from the second 24mer could then be selected and compared for similarity against the first chosen sequence: GTTAGAGTTAATTGTATTGATGA (SEQ ID NO:2). A systematic pairwise comparison could then be carried out to determine if the similarity requirements are violated. If the pair of sequences does not violate any set property, a 10mer subsequence can be selected from the third 24mer sequence of Table I, and compared to each of the first two 10mer sequences (in a pairwise fashion to determine its compatibility therewith, etc. In this way a family of 10mer sequences may be developed.

It is within the scope of this invention, to obtain families of sequences containing 11mer, 12mer, 13mer, 14mer, 15mer, 16mer, 17mer, 18mer, 19mer, 20mer, 21mer, 22mer and 23mer sequences by analogy to that shown for 10mer sequences.

It may be desirable to have a family of sequences in which there are sequences greater in length than the 24mer sequences shown in Table I. It is within the capability of a person skilled in the art, given the family of sequences shown in Table I, to obtain such a family of sequences. One possible approach would be to insert into each sequence at one or more locations a nucleotide, non-natural base or analogue such that the longer sequence should not have greater similarity than any two of the original non-cross-hybridizing sequences of Table I and the addition of extra bases to the tag sequences should not result in a major change in the thermodynamic properties of the tag sequences of that set for example the GC content must be maintained between 10%-40% with a variance from the average of 20%. This

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method of inserting bases could be used to obtain, for example, a family of sequences up to 40 bases long.

Given a particular family of sequences that can be used as a family of tags (or tag complements), e.g., those of Table I, a skilled person will readily recognize variant families that work equally as well.

Again taking the sequences of Table I for example, every T could be converted to an A and vice versa and no significant change in the cross-hybridization properties would be expected to be observed. This would also be true if every G were converted to a C.

Also, all of the sequences of a family could be taken to be constructed in the 5'-3' direction, as is the convention, or all of the constructions of sequences could be in the opposition direction (3'-5').

There are additional modifications that can be carried out. For example, C has not been used in the family of sequences. Substitution of C in place of one or more G's of a particular sequence would yield a sequence that is at least as low in homology with every other sequence of the family as was the particular sequence chosen for modification. It is thus possible to substitute C in place of one or more G's in any of the sequences shown in Table I. Analogously, substituting of C in place of one or more A's is possible, or substituting C in place of one or T's is possible.

It is preferred that the sequences of a given family are of the same, or roughly the same length. Preferably, all the sequences of a family of sequences of this invention have a length that is within five bases of the base-length of the average of the family. More preferably, all sequences are within four bases of the average base-length. Even more preferably, all or almost all sequences are within three bases of the average base-length of the family. Better still, all or almost all sequences have a length that is within two of the base-length of the average of the family, and even better still, within one of the base-length of the average of the family.

It is also possible for a person skilled in the art to derive sets of sequences from the family of sequences described in this specification and remove sequences that would be expected to have undesirable hybridization properties.

#### Methods For Synthesis Of Oligonucleotide Families

Preferably oligonucleotide sequences of the invention are synthesized directly by standard phosphoramidite synthesis approaches and the like (Caruthers et al, Methods in Enzymology; 154, 287-313: 1987; Lipshutz et al, Nature Genet.; 21, 20-24: 1999; Fodor et al, Science; 251, 763-773: 1991). Alternative chemistries involving non

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natural bases such as peptide nucleic acids or modified nucleosides that offer advantages in duplex stability may also be used (Hacia et al; Nucleic Acids Res ;27: 4034-4039, 1999; Nguyen et al, Nucleic Acids Res.;27, 1492-1498: 1999; Weiler et al, Nucleic Acids Res.; 25, 2792-2799:1997). It is also possible to synthesize the oligonucleotide sequences of this invention with alternate nucleotide backbones such as phosphorothioate or phosphoroamidate nucleotides. Methods involving synthesis through the addition of blocks of sequence in a stepwise manner may also be employed (Lyttle et al, Biotechniques, 19: 274-280 (1995). Synthesis may be carried out directly on the substrate to be used as a solid phase support for the application or the oligonucleotide can be cleaved from the support for use in solution or coupling to a second support.

#### Solid Phase Supports

There are several different solid phase supports that can be used with the invention. They include but are not limited to slides, plates, chips, membranes, beads, microparticles and the like. The solid phase supports can also vary in the materials that they are composed of including plastic, glass, silicon, nylon, polystyrene, silica gel, latex and the like. The surface of the support is coated with the complementary tag sequences by any conventional means of attachment.

In preferred embodiments, the family of tag complement sequences is derivatized to allow binding to a solid support. Many methods of derivatizing a nucleic acid for binding to a solid support are known in the art (Hermanson G., Bioconjugate Techniques; Acad. Press: 1996). The sequence tag may be bound to a solid support through covalent or non-covalent bonds (Iannone et al, Cytometry; 39: 131-140, 2000; Matson et al, Anal. Biochem.; 224: 110-106, 1995; Proudnikov et al, Anal Biochem; 259: 34-41, 1998; Zammattéo et al, Analytical Biochemistry; 280:143-150, 2000). The sequence tag can be conveniently derivatized for binding to a solid support by incorporating modified nucleic acids in the terminal 5' or 3' locations.

A variety of moieties useful for binding to a solid support (e.g., biotin, antibodies, and the like), and methods for attaching them to nucleic acids, are known in the art. For example, an amine-modified nucleic acid base (available from, eg., Glen Research) may be attached to a solid support (for example, Covalink-NH, a polystyrene surface grafted with secondary amino groups, available from Nunc) through a bifunctional crosslinker (e.g., bis(sulfosuccinimidyl suberate), available from Pierce). Additional spacing

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moieties can be added to reduce steric hindrance between the capture moiety and the surface of the solid support.

#### Attaching Tags to Analytes for Sorting

5 A family of oligonucleotide tag sequences can be conjugated to a population of analytes most preferably polynucleotide sequences in several different ways including but not limited to direct chemical synthesis, chemical coupling, ligation, amplification, and the like. Sequence tags that have been synthesized with primer sequences can be used for enzymatic  
10 extension of the primer on the target for example in PCR amplification.

#### Detection of Single Nucleotide Polymorphisms Using Primer Extension

There are a number of areas of genetic analysis where families of non-cross-hybridizing sequences can be applied including disease diagnosis, single  
15 nucleotide polymorphism analysis, genotyping, expression analysis and the like. One such approach for genetic analysis, referred to as the primer extension method (also known as Genetic Bit Analysis (Nikiforov et al, Nucleic Acids Res.; 22, 4167-4175: 1994; Head et al Nucleic Acids Res.; 25, 5065-5071: 1997)), is an extremely accurate method for identification of the nucleotide  
20 located at a specific polymorphic site within genomic DNA. In standard primer extension reactions, a portion of genomic DNA containing a defined polymorphic site is amplified by PCR using primers that flank the polymorphic site. In order to identify which nucleotide is present at the polymorphic site, a third primer is synthesized such that the polymorphic position is located  
25 immediately 3' to the primer. A primer extension reaction is set up containing the amplified DNA, the primer for extension, up to 4 dideoxynucleoside triphosphates (each labeled with a different fluorescent dye) and a DNA polymerase such as the Klenow subunit of DNA Polymerase 1. The use of dideoxy nucleotides ensures that a single base is added to the 3'  
30 end of the primer, a site corresponding to the polymorphic site. In this way the identity of the nucleotide present at a specific polymorphic site can be determined by the identity of the fluorescent dye-labeled nucleotide that is incorporated in each reaction. One major drawback to this approach is its low throughput. Each primer extension reaction is carried out independently in a  
35 separate tube.

Universal sequences can be used to enhance the throughput of primer extension assay as follows. A region of genomic DNA containing multiple polymorphic sites is amplified by PCR. Alternatively, several genomic regions containing one or more polymorphic sites each are amplified  
40 together in a multiplexed PCR reaction. The primer extension reaction

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is carried out as described above except that the primers used are chimeric, each containing a unique universal tag at the 5' end and the sequence for extension at the 3' end. In this way, each gene-specific sequence would be associated with a specific universal sequence. The chimeric primers would be hybridized to the amplified DNA and primer extension is carried out as described above. This would result in a mixed pool of extended primers, each with a specific fluorescent dye characteristic of the incorporated nucleotide. Following the primer extension reaction, the mixed extension reactions are hybridized to an array containing probes that are reverse complements of the universal sequences on the primers. This would segregate the products of a number of primer extension reactions into discrete spots. The fluorescent dye present at each spot would then identify the nucleotide incorporated at each specific location. A number of additional methods for the detection of single nucleotide polymorphisms, including but not limited to, allele specific polymerase chain reaction (ASPCR), allele specific primer extension (ASPE) and oligonucleotide ligation assay (OLA) can be performed by someone skilled in the art in combination with the tag sequences described herein.

#### Kits Using Families Of Tag Sequences

The families of non cross-hybridizing sequences may be provided in kits for use in for example genetic analysis. Such kits include at least one set of non-cross-hybridizing sequences in solution or on a solid support. Preferably the sequences are attached to microparticles and are provided with buffers and reagents that are appropriate for the application. Reagents may include enzymes, nucleotides, fluorescent labels and the like that would be required for specific applications. Instructions for correct use of the kit for a given application will be provided.

#### EXAMPLES

##### EXAMPLE 1 - Cross Talk Behavior of Sequence on Beads

A group of 100 sequences, randomly selected from Table I, was tested for feasibility for use as a family of minimally cross-hybridizing oligonucleotides. The 100 sequences selected are separately indicated in Table I along with the numbers assigned to the sequences in the tests.

The tests were conducted using the Luminex LabMAP™ platform available from Luminex Corporation, Austin, Texas, U.S.A. The one hundred sequences, used as probes, were synthesized as oligonucleotides by Integrated DNA Technologies (IDT, Coralville, Iowa, U.S.A.). Each probe included a C<sub>6</sub>



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aminolink group coupled to the 5'-end of the oligonucleotide through a C<sub>12</sub> ethylene glycol spacer. The C<sub>6</sub> aminolink molecule is a six carbon spacer containing an amine group that can be used for attaching the oligonucleotide to a solid support. One hundred oligonucleotide targets (probe complements), the sequence of each being the reverse complement of the 100 probe sequences, were also synthesized by IDT. Each target was labelled at its 5'-end with biotin. All oligonucleotides were purified using standard desalting procedures, and were reconstituted to a concentration of approximately 200 µM in sterile, distilled water for use. Oligonucleotide concentrations were determined spectrophotometrically using extinction coefficients provided by the supplier.

Each probe was coupled by its amino linking group to a carboxylated fluorescent microsphere of the LapMAP system according to the *Luminex*<sup>100</sup> protocol. The microsphere, or bead, for each probe sequence has unique, or spectrally distinct, light absorption characteristics which permits each probe to be distinguished from the other probes. Stock bead pellets were dispersed by sonication and then vortexing. For each bead population, five million microspheres (400 µL) were removed from the stock tube using barrier tips and added to a 1.5 mL Eppendorf tube (USA Scientific). The microspheres were then centrifuged, the supernatant was removed, and beads were resuspended in 25 µL of 0.2 M MES (2-(N-morpholino)ethane sulfonic acid) (Sigma), pH 4.5, followed by vortexing and sonication. One nmol of each probe (in a 25 µL volume) was added to its corresponding bead population. A volume of 2.5 µL of EDC cross-linker (1-ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (Pierce), prepared immediately before use by adding 1.0 mL of sterile ddH<sub>2</sub>O to 10 mg of EDC powder, was added to each microsphere population. Bead mixes were then incubated for 30 minutes at room temperature in the dark with periodic vortexing. A second 2.5 µL aliquot of freshly prepared EDC solution was then added followed by an additional 30 minute incubation in the dark. Following the second EDC incubation, 1.0 mL of 0.02% Tween-20 (BioShop) was added to each bead mix and vortexed. The microspheres were centrifuged, the supernatant was removed, and the beads were resuspended in 1.0 mL of 0.1% sodium dodecyl sulfate (Sigma). The beads were centrifuged again and the supernatant removed. The coupled beads were resuspended in 100 µL of 0.1 M MES pH 4.5. Bead concentrations were then determined by diluting each preparation 100-fold in ddH<sub>2</sub>O and enumerating using a

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Neubauer BrightLine Hemacytometer. Coupled beads were stored as individual populations at 8°C protected from light.

The relative oligonucleotide probe density on each bead population was assessed by Terminal Deoxynucleotidyl Transferase (TdT) end-labelling with biotin-ddUTPs. TdT was used to label the 3'-ends of single-stranded DNA with a labeled ddNTP. Briefly, 180 µL of the pool of 100 bead populations (equivalent to about 4000 of each bead type) to be used for hybridizations was pipetted into an Eppendorf tube and centrifuged. The supernatant was removed, and the beads were washed in 1x TdT buffer. The beads were then incubated with a labelling reaction mixture, which consisted of 5x TdT buffer, 25mM CoCl<sub>2</sub>, and 1000 pmol of biotin-16-ddUTP (all reagents were purchased from Roche). The total reaction volume was brought up to 85.5 µL with sterile, distilled H<sub>2</sub>O, and the samples were incubated in the dark for 1 hour at 37°C. A second aliquot of enzyme was added, followed by a second 1 hour incubation. Samples were run in duplicate, as was the negative control, which contained all components except the TdT. In order to remove unincorporated biotin-ddUTP, the beads were washed 3 times with 200 µL of hybridization buffer, and the beads were resuspended in 50 µL of hybridization buffer following the final wash. The biotin label was detected spectrophotometrically using SA-PE (streptavidin-phycoerythrin conjugate). The streptavidin binds to biotin and the phycoerythrin is spectrally distinct from the probe beads. The 10mg/mL stock of SA-PE was diluted 100-fold in hybridization buffer, and 15 µL of the diluted SA-PE was added directly to each reaction and incubated for 15 minutes at 37°Celsius. The reactions were analyzed on the *Luminex*<sup>100</sup> LabMAP. Acquisition parameters were set to measure 100 events per bead using a sample volume of 50 µL.

The results obtained are shown in Figure 2. As can be seen the Mean Fluorescent Intensity (MFI) of the beads varies from 840.3 to 3834.9, a range of 4.56-fold. Assuming that the labelling reactions are complete for all of the oligonucleotides, this illustrates the signal intensity that would be obtained for each type of bead at this concentration if the target (i.e., labelled complement) was bound to the probe sequence to the full extent possible.

The cross-hybridization of targets to probes was evaluated as follows. 100 oligonucleotide probes linked to 100 different bead populations, as described above, were combined to generate a master bead mix, enabling multiplexed reactions to be carried out. The pool of

microsphere-immobilized probes was then hybridized individually with each biotinylated target. Thus, each target was examined individually for its specific hybridization with its complementary bead-immobilized sequence, as well as for its non-specific hybridization with the other 99 bead-immobilized universal sequences present in the reaction. For each hybridization reaction, 25  $\mu$ L bead mix (containing about 2500 of each bead population in hybridization buffer) was added to each well of a 96-well Thermowell PCR plate and equilibrated at 37°C. Each target was diluted to a final concentration of 0.002 fmol/ $\mu$ L in hybridization buffer, and 25  $\mu$ L (50 fmol) was added to each well, giving a final reaction volume of 50  $\mu$ L. Hybridization buffer consisted of 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 and hybridizations were performed at 37°C for 30 minutes. Each target was analyzed in triplicate and six background samples (i.e. no target) were included in each plate. A SA-PE conjugate was used as a reporter, as described above. The 10 mg/mL stock of SA-PE was diluted 100-fold in hybridization buffer, and 15  $\mu$ L of the diluted SA-PE was added directly to each reaction, without removal of unbound target, and incubated for 15 minutes at 37°C. Finally, an additional 35  $\mu$ L of hybridization buffer was added to each well, resulting in a final volume of 100  $\mu$ L per well prior to analysis on the Luminex<sup>100</sup> LabMAP. Acquisition parameters were set to measure 100 events per bead using a sample volume of 80  $\mu$ L.

The percent hybridization was calculated for any event in which the NET MFI was at least 3 times the zero target background. In other words, a calculation was made for any sample where  $(\text{MFI}_{\text{sample}} - \text{MFI}_{\text{zero target background}}) / \text{MFI}_{\text{zero target background}} \geq 3$ .

The net median fluorescent intensity  $(\text{MFI}_{\text{sample}} - \text{MFI}_{\text{zero target background}})$  generated for all of the 10,000 possible target/probe combinations was calculated. As there are 100 probes and 100 targets, there are  $100 \times 100 = 10,000$  possible different interactions possible of which 100 are the result of perfect hybridizations. The remaining 9900 result from hybridization of a target with a mismatched probe. A cross-hybridization event is then defined as a non-specific event whose net median fluorescent intensity exceeds 3 times the zero target background. In other words, a cross-talk calculation is only be made for any sample where  $(\text{MFI}_{\text{sample}} - \text{MFI}_{\text{zero target background}}) / \text{MFI}_{\text{zero target background}} \geq 3$ . Cross-hybridization events were quantified by expressing the value of the cross-hybridization signal as a percentage of the perfect match hybridization signal with the same probe.

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The results obtained are illustrated in Figure 3. The ability of each target to be specifically recognized by its matching probe is shown. Of the possible 9900 non-specific hybridization events that could have occurred when the 100 targets were each exposed to the pool of 100 probes, 6 events were observed. Of these 6 events, the highest non-specific event generated a signal equivalent to 5.3% of the signal observed for the perfectly matched pair (i.e. specific hybridization event).

Each of the 100 targets was thus examined individually for specific hybridization with its complement sequence as incorporated onto a microsphere, as well as for non-specific hybridization with the complements of the other 99 target sequences. Representative hybridization results for target (complement of probe 90, Table I) are shown in Figure 4. Probe 90 was found to hybridize only to its perfectly-matched target. No cross-hybridization with any of the other 99 targets was observed.

The foregoing results demonstrate the possibility of incorporating the 1168 sequences of Table I, or any subset thereof, into a multiplexed system with the expectation that most if not all sequences can be distinguished from the others by hybridization. That is, it is possible to distinguish each target from the other targets by hybridization of the target with its precise complement and minimal hybridization with complements of the other targets.

#### EXAMPLE 2 - Tag sequences used in sorting polynucleotides

The family of non cross hybridizing sequence tags or a subset thereof can be attached to oligonucleotide probe sequences during synthesis and used to generate amplified probe sequences. In order to test the feasibility of PCR amplification with non cross hybridizing sequence tags and subsequently addressing each respective sequence to its appropriate location on two-dimensional or bead arrays, the following experiment was devised. A 24mer tag sequence can be connected in a 5'-3' specific manner to a p53-exon specific sequence (20mer reverse primer). The connecting p53 sequence represents the inverse complement of the nucleotide gene sequence. To facilitate the subsequent generation of single stranded DNA post-amplification the tag-Reverse primer can be synthesized with a phosphate modification ( $\text{PO}_4$ ) on the 5'-end. A second PCR primer can also be generated for each desired exon, represented by the Forward (5'-3') amplification primer. In this instance the Forward primer can be labeled with a 5'-biotin modification to allow detection with Cy3-avidin or equivalent.

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A practical example of the aforementioned description is as follows:  
For exon 1 of the human p53 tumor suppressor gene sequence the following tag-Reverse primer (SEQ ID NO:1171) can be generated:

5 222087 222063  
5'-PO4-ATGTTAAAGTAAGTGTGAAATGT -TCCAGGGAAGCGTGTACCGTCGT-3'  
Tag Sequence # 3 Exon 1 Reverse

The numbering above the Exon-1 reverse primer represents the genomic nucleotide positions of the indicated bases.

The corresponding Exon-1 Forward primer sequence (SEQ ID NO:1172) is as follows:

221873 221896

15 5'-Biotin-TCATGGCGACTGTCCAGCTTTGTG-3'

In combination these primers will amplify a product of 214 bp plus a 24 bp tag extension yielding a total size of 238 bp.

Once amplified, the PCR product can be purified using a QIAquick PCR purification kit and the resulting DNA can be quantified. To generate single stranded DNA, the DNA is subjected to  $\lambda$ -exonuclease digestion thereby resulting in the exposure of a single stranded sequence (anti-tag) complementary to the tag-sequence covalently attached to the solid phase array. The resulting product is heated to 95°C for 5 minutes and then directly applied to the array at a concentration of 10-50 nM. Following hybridization and concurrent sorting, the tag-Exon 1 sequences are visualized using Cy3-streptavidin. In addition to direct visualization of the biotinylated product, the product itself can now act as a substrate for further analysis of the amplified region, such as SNP detection and haplotype determination.

## DEFINITIONS

**Non-cross-hybridization:** Describes the absence of hybridization between  
35 two sequences that are not perfect complements of each other.

**Cross-hybridization:** The hydrogen bonding of a single-stranded DNA sequence that is partially but not entirely complementary to a single-stranded substrate.

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**Homology or Similarity:** How closely related two or more separate strands of DNA are to each other, based on their base sequences.

**Analogue:** The symbols A, G, T/U, C take on their usual meaning in the art here. In the case of T and U, a person skilled in the art would understand that these are equivalent to each other with respect to the inter-strand hydrogen-bond (Watson-Crick) binding properties at work in the context of this invention. The two bases are thus interchangeable and hence the designation of T/U. A chemical, which resembles a nucleotide base is an analogue thereof. A base that does not normally appear in DNA but can substitute for the ones, which do, despite minor differences in structure. Analogues particularly useful in this invention are of the naturally occurring bases can be inserted in their respective places where desired. Such an analogue is any non-natural base, such as peptide nucleic acids and the like that undergoes normal Watson-Crick pairing in the same way as the naturally occurring nucleotide base to which it corresponds.

**Complement:** The opposite or "mirror" image of a DNA sequence. A complementary DNA sequence has an "A" for every "T" and a "C" for every "G". Two complementary strands of single stranded DNA, for example a tag sequence and its complement, will join to form a double-stranded molecule.

**Complementary DNA (cDNA):** DNA that is synthesized from a messenger RNA template; the single-stranded form is often used as a probe in physical mapping.

**Oligonucleotide:** Refers to a short nucleotide polymer whereby the nucleotides may be natural nucleotide bases or analogues thereof.

**Tag:** Refers to an oligonucleotide that can be used for specifically sorting analytes with at least one other oligonucleotide that when used together do not cross hybridize.

Table I

Sequence	SEQ ID NO:	No. in Ex 1
A A A T T G T G A A A G A T T G T T T G T G T A	1	1
G T T A G A G T T A A T T G T A T T T G A T G A	2	-
A T G T T A A A G T A A G T G T T G A A A T G T	3	-
T G A T G T T A G A A G T A T A T T G T G A A T	4	-
T T T G T G T A G A A T A T G T G T T G T T A A	5	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
A T A A G T G T A A G T G A A A T A A G A A G A	6	-
A A G A G T A T T T G T T G T G A G T T A A A T	7	-
G T G T T T A T G T T A T A T G T G A A G T T T	8	-
A A A G A G A A T A G A A T A T G T G T A A G T	9	-
T A T G A A A G A G T G A G A T A A T G T T T A	10	-
A T G A G A A A T A T G T T A G A A T G T G A T	11	-
T T A G T T G T T G A T G T T T A G T A G T T T	12	-
G T A A A G A G T A T A A G T T T G A T G A T A	13	-
A A A G T A A G A A T G A T G T A A T A A G T G	14	-
G T A G A A A T A G T T T A T T G A T G A T T G	15	-
T G T A A G T G A A A T A G T G A G T T A T T T	16	2
A A A T A G A T G A T A T A A G T G A G A A T G	17	-
A T A A G T T A T A A G T T A T G T G A G T	18	-
T A T A G A T A A A G A G A T G A T T T G T T G	19	-
A G A G T T G A G A A T G T A T A G T A T T A T	20	-
A A G T A G T T T G T A A G A A T G A T T G T A	21	-
T T A T G A A A T T G A G T G A A G A T T G A T	22	-
G T A T A T G T A A A T T G T T A T G T T G A G	23	-
G A A T T G T A T A A A G T A T T A G A T G T G	24	4
T A G A T G A G A T T A A G T G T T A T T T G A	25	-
G T T A A G T T T G T T T A T G T A T A G A A G	26	-
G A G T A T T A G T A A A G T G A T A T G A T A	27	-
G T G A A T G A T T T A G T A A A T G A T T G A	28	-
G A T T G A A G T T A T A G A A A T G A T T A G	29	-
A G T G A T A A A T G T T A G T T G A A T T G T	30	-
T A T A T A G T A A A T G T T T G T G T G T T G	31	-
T T A A G T G T T A G T T A T T T G T T G T A G	32	-
G T A G T A T A T A G A A G T G A G A A T A T A	33	-
T A G T G T A T A G A A A T G T A G A T T T A G T	34	-
T T G T A G A T T A G A T G T G T T T G T A A A	35	-
T A G T A T A G A G T A G A G A T G A T A T T T	36	-
A T T G T G A A A G A A A G A G A A A A T T	37	7
T G T G A G A A T T A A G A T T A A G A A T G T	38	-
A T A T T A G T T A A G A A A G A A G A G T T G	39	-
T T G T A G T T G A G A A A T A T G T A G T T T	40	-
T A G A G T T G T T A A A G A G T G T A A A T A	41	-
G T T A T G A T G T G T A T A A G T A A T A T G	42	-
T T T G T T A G A A A T G A G A A G A T T T A T G	43	10
A G T A T A G T T T A A A G A A G T A G T A G A	44	-
G T G A G A T A T A G A T T T A G A A A G T A A	45	-
T T G T T T A T A G T G A A G T G A A T A G T A	46	-
A A G T A A G T A G T A A T A G T G T G T T A A	47	-
A T T T G T G A G T T A T G A A A G A T A A G A	48	-
G A A A G T A G A G A A T A A A G A T A A G A A	49	-
A T T T A A G A T T G T T A A G A G T A G A A G	50	-
G T T T A A A G A T T G T A A G A A T G T G T A	51	-
T T T G T G A A G A T G A A G T A T T T G T A T	52	-
T G T G T T T A G A A T T T A G T A T G T G T A	53	-
G A T A A T G A T T A T A G A A A G T G T T T G	54	-
G T T A T T T G T A A G T T A A G A T A G T A G	55	-
A G T T T A T T G T A A A G A G T T T G A A T A G	56	-
T T G T G T T T A T T G T G T A G T T T A A A G	57	-
A T T G T G A G A A G A T A T G A A A G T T A T	58	-
T G A G A A T G T A A A G A A T G T T T A T T G	59	13
A T G T G A A A G T T A T G A T G T T A A T T G	60	-
G T T T A G T A T T A G T T G T T A A G A T T G	61	-
G A T T G A T A T T T G A A T G T T T G T T T G	62	14

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
TGAAATTGAAAGTGTAAATGTTGTAT	63	-
GATTTGTATTGTTGAGAAATAGAAATA	64	-
AAAATTTGAGATTGTTGTATAGAGTA	65	-
GTAATTAGATTGTTGTGTTGTGTTGT	66	-
GTTTGTATTGTTAGTGAATATAGT	67	-
ATGTAGTAGTAGATGTTTATGAAAT	68	-
TGTTTAAAGATGATTGAAAGAAATG	69	-
TGTGATAATGATGTTATTTGTGTA	70	-
ATAGTTGTGAGAAATTTGTTAATTAG	71	-
ATAGATGTAAAGAGAAATTTGTGAAA	72	-
AGATTAAAGAGAAAGTTAATAGAGTA	73	-
GAAAGTAAATTTGTGAATGAAAGAAA	74	-
AATGTAAAGAAAGAAAGATTGTTGTA	75	-
TTTGATTATTATGTTGTTATGTTGAGT	76	-
GTAATTGAGAAATTTGAAAGAAATGAA	77	-
GAAATTGTATGAAATGAAATTTGTAAG	78	-
TATTTGTAGAAAGTAAAGTTAGAAAGT	79	-
TTTATAGTAAATGATAAGTGTAGTTG	80	-
ATAATAGTTGAAATTTGTGATAGTTGT	81	-
ATAAGAAATTTAGAGAGTTGTAAGAG	82	-
GAAATTTGTGAAATGTTGATATATA	83	-
AAATAAGTAGATTTAATGAGAGAAAG	84	-
GATTAAAGAAAGTAAAGTGAATGTTT	85	-
TATGTGTGTTTGTGTTTAGTGTATTAA	86	-
GAGTTTATATGTAGTTTAGAGTTATA	87	-
GAAAGAAAGAAAGTGTTAAGTTTAAA	88	-
TAGTATTAGTAAAGTATGTGATTGT	89	-
TTGTGTGATTGAAATATTGTGAAAT	90	-
ATGTGTAAGAGATTAAAGTATTAAA	91	-
GATTGAAATGATTGAGATATGTAAA	92	-
AAGATGATAGTTTAAAGTGTAAAGTTA	93	17
TAGTTGTATTATTGAGAAATTTAGAAAG	94	-
TTTATAGTGAATTTATGAGTGAAGAG	95	-
GATAGATTTTAGAAATGAATTAAGTG	96	18
TTTGAAGAAAGAGATTTCGAAATTTGA	97	-
ATGAATAAGAGATTGATAAAATGTGA	98	-
TGTTTATGTAGTGTGATGAAATTT	99	-
TTTAAAGTGAAGTTATAGAAAGTAGTA	100	19
GATTTTATGTGTTTGAAGTTAAGAT	101	-
TAGTTAGAGAAAGTGTATAAGTTTA	102	-
GTAATGATAAATGAAGTGTATATAG	103	-
AATGAAGTGTATTAGTATAGATAGTA	104	-
TAAATTGTGAGTTTGTGTTTGAATTGTAG	105	-
TAAATGAAGAAATAGTATGAGTGT	106	-
AAATGTAAATAGTGTGTTAGTTAG	107	-
AGAGTTAGTGAATAAGTTGTTAAAT	108	-
GAAATAGAAATGTATTGTTTGTGA	109	-
AGTTATTAAGTTTGTGAGAAATTAAG	110	-
GAGTTTATAGTTTGAATAATGTTGT	111	-
AGAGTTATTAGAAAGAAAGATTTAAG	112	-
GAGTTTAAATGAATAAGTATTGTTG	113	-
ATGATGAATAGTGTGAAAGTATATAG	114	-
ATAGATATGAGATGAAAGTTAGTA	115	-
TATGTAAAGAAAGTGAAGAAAGAA	116	-
TGAATGTAGAAATGAATGTTGAAA	117	-
AATTGAATAGTGTGTGAGTTTAAAT	118	-
AGATATTGTTTGAATTAATGAAGAG	119	-



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Table I

Sequence	SEQ ID NO:	No. in Ex 1
A A A G T T G T A A A G T T G A A G A T A A A G	120	-
G T T A A G A G A T T A T G A G A T G T A T T A	121	-
A G A A G A T A T A A G A A G A T T G A A T T G	122	-
G T A G A A A T T T G A A T T G A T G T G A A A	123	-
A A G A G T A G A T T G A T A A G T A T A T G A	124	-
T G A T A T A G T A G T G A A G A A A T A A G T	125	22
A G A T A A A T G A T G A G A A A T G A A G A T A	126	-
A T G T G A A A G T A T T T G T G A T A T A G T	127	-
A A T A A G A G A A T T G A T A T G A A G A T G	128	23
T A A G T G T A T T T A G T A G A A T G A A G T	129	-
T A T G T T A G A T T T G T T G A G A T T G A T	130	-
A G T T T G T A T G A A G A G A T A G T A T T T	131	-
G A G A A A T G T T A T G T A T T T A G T A G T	132	-
T A T G T G A G A A T G T G T T T G A T T T T A A	133	-
G T A T G T T T G T T T A T A G A A A T G T A T G	134	-
G A G T A T A T A G A A G A A A G A A A T T T G	135	-
A T G A G T G A A G T A A A T G T A G T T A T T	136	-
T T A A G A A G T G A G T T A T T G T G A T A T	137	-
A T G A A A T G A G A A T A T T G T T G T T T G	138	-
G A T T A A T G A T T A T G T G A A T T G A T G	139	-
G A A A T G T T A A A G A T A T G A A A G T A G	140	-
T A T T G T T G A T T T G A T A T T A G T G T G	141	-
T T T A T G T T T G T G T A T G T A A G T A G T	142	-
A A T T G A A A G A A A T T G T G T G A A T T G A	143	-
T G A G T T T G A A T T T G T T T G A G T A A T	144	-
G A T G T A T A A T G A T G T G T G T A A A T T	145	-
A T G T G A G A G A A G A A T T T G T T T A T T	146	-
G T G A T A A A G T A T T G T T G A T A G A A A	147	-
G A A G T A G A A T A G A A A G T T A A T A G A	148	-
T T G T G T A G T T A A G A G T T G T T T A A T	149	24
T A G T A G T A A G T T G T T A G A A T A G T T	150	-
A A T T T G A A G T A T A A T G A A T G T G T G	151	-
T A G A A A T T G T A G T A T T T G A G A G A A	152	-
T G T A T A T G T T A A T G A G A T G T T G T A	153	25
T A T T T G A T A A G A G A A T G A A G A A G T	154	26
T T G A A T A G T G T A A T G A A T A T G A T G	155	-
G T A G T T T T G T G A A T A G A A T T A G T T T	156	-
A A A G A T G A T T G T A A T T T G T G T G A A	157	-
G A A G A T T G T T G A G T T A A T A G A T A A	158	-
A G A T T A T G T A G T G A T G T A A A T G T T	159	-
G A A T T T A G A T G T A G A T A T G A A T G T	160	-
G A T A G A A G T G T A T T A A G T A A G T T A	161	-
T A T G A A T T A T G A G A A G A A T A G A G T	162	-
T T T G T T A T G A A G T G A T T T T G T T T G T	163	-
G T A A A G A T T G T G T T A T A T G A A A T G	164	-
T T G T G A T A G T A G T T A G A T A T T T G T	165	28
G A A T T A A G A T A A A G A A G A G A A G T A	166	-
G A T T G T A G A A T G A A T T T G T A G T A T	167	-
A A A T A A G A G A G A G A A T G A T T T A G T	168	-
A A T T A T G T G A A T A G A T T G T T G A A G	169	-
T T A A G A T T T A T G T G A T A G T A G A G T	170	-
T T A A A G A T T A G T G T T T G T G T G T A	171	-
T A T T G A T T T A T G A A G A G T A T A G T G	172	-
A A A T T T G A T G A G T A G T T T A A G A G A	173	-
A T A A A G T T G T T T G A T G T T T G A A T G	174	-
G A T T G T G A T G A A T A A T G T T A T T G A	175	-
G A T G A A G A A A T A T G A T A T G A A T A G	176	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
TTAAAGTTATTGAAAGTGAAGTTGA	177	-
TTGTAAAGAAATAGAGATTGTTGTT	178	-
GAGATTGAGTTTAAGTATTAGATT	179	-
AGTGATAATAGAAATGATAAATGTG	180	-
GATAAATAGTGAAATTTGAGTTGTAT	181	-
AGATAATTGTTAGTAGAAGTATGT	182	-
GTTATGAATGTTGAATTTGAATGT	183	-
ATGAAGAATTTAGTTGTGAGATAT	184	30
AAATAGAGAAAGTTATGATGTGATA	185	-
TTAGTGAGAAATGTTTAAATGTGAT	186	-
TGAAGAAATATGTTGAATTAGTTTG	187	-
GTTTGTAGATTTTAATGAGTATTGA	188	-
GTTGTAAAGTAAATGATAAAGTATGA	189	-
TAAAGTAGTAGTAATTGTTTAGA	190	-
TTTGAGAGAGTAGTATGATTATTT	191	-
ATTGATTGTGAATTAGATAGAAAGA	192	-
GATTAGTATTTAGTAGTAATAGAG	193	31
TATGTATTTAGAGATAATTGAAAGTG	194	-
TATGTGAAGAAGTAATGATAAATGAG	195	-
GTAATTAGTAATGATTTGAAATGAG	196	-
GTTTATTTGTAAAGATGTAAGTGAA	197	-
TAGTAGAAATTGTTGTTAAAGAAATG	198	32
TATTTGTTAGTTATGTTAGTGTGTA	199	-
GAGTGAAAGTTATATGAAAGTATA	200	-
ATATAGAAAGTTGATGAGTTTATGA	201	-
TTTAGAAAGTAAGAAATAAGTGAGTA	202	-
TGTGTATTAAGATAATTGTTAAGAAAG	203	-
TAGAAAGAGTTGTATTTGTTATAAGT	204	-
GTGTTATATTAGTTTAAAGTTAGAGTA	205	-
AAATATAGTGTGATGTGAATTTGAATG	206	-
TTAGAGAAATAGAGTGATTTATAGTT	207	-
GAAAGTGAGTTAAATGATTTGTAAAT	208	-
AAATGTAAAGTAAGAAAGTGATGA	209	33
GTTTAGTTATGATGAATATTGTGTA	210	34
AAATGAGTTAGAGTAGAAATTATGT	211	-
GATATAGAAAGATTAGTTTAGTGATA	212	-
ATAGTTTGTGAGATTATGAGTA	213	-
TAGAAATAGTTAGTAGTAAGAGTAT	214	-
GAAATTTGTATTTGTGAAGTTTAGTA	215	-
GTAGTAAGAAAGAGAAATTAGATTAA	216	-
AAATGTGTTATGTAATGTAATAAGTG	217	-
GAAATTAGTTAGAGTAATAATTGTTTG	218	-
GAAATTGAAAGATAGTAAGAAATGA	219	-
GTGTATTATGTTGATTTATGATAGA	220	-
TATTTATGAGAAAGATTGAATAGTAG	221	35
TATGTATTGTATTGAGTAGATGAA	222	-
GTGATTGAAATAGTAGATTGTTTAA	223	36
AGTAAGTTGTTTGTATTGAAATTTTG	224	-
GAAAGTTTGTATTTAAGTTTAAGAAAG	225	-
GAGAAAGATAAATGATATTGTTATG	226	-
ATGATGAGTTGTTAATAGTTAGTT	227	-
TATGATATTGTAAGAGTGTTAAGA	228	-
GAGATGATTTAAAGTGATTTATGAA	229	-
ATAGTTAAAGAGTGATGAGATAAAA	230	-
TTTATTGTTAGATAAAGAGTTGAG	231	-
AGAAATATTGATAGTTTGAAGTTGAA	232	-
TAGTGTAAAGTGATGATTTGTAAAT	233	-

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Sequence	SEQ ID NO:	No. in Ex 1
A G T A G T G A T A T G A T T T G A A T A T T G	234	-
T G T A T T G A A T T A G A A T A G T G A G A A	235	-
T G A T A T G A G A T A G A A G T T T A A T G T	236	-
G A A G A A G T A A G T A T A A G T A A A T G	237	-
T T T A A G T G T G A T A A G A A A G A T A G A	238	-
T A T T G T T G A A T G T G T T T A A A G A G A	239	38
G A A T A A T G A T G A G A T G A T T A T T G A	240	-
T A G A G A A A G A G A G A A T T G T A T T A A	241	39
A T G T A T A A T G A G A T A T G T T T G T G A	242	-
A A T A G A T A A G A T T G A T T G T G T T T G	243	40
T T T G A T G A T A A T A G A A G A G A A T G A	244	-
A G A T G A A T A A G T T G T G A A T G T T T A	245	-
A G A T G A A A G A A A G T G T A G A A T A T T	246	-
T G T T A A A T G T A T G T A G T A A T T G A G	247	41
T A G T A G T G T G A A G T T A T T T G T T A T	248	-
A G T G A A T G T T T G T A A A G A G T T T A A	249	-
G A T A A A T G A G A A T T G A G T A A T T G T	250	-
T G A T G A G A A A T T G T T T A A G T G T T T	251	-
A A A T A A G T A G T G T G A G T A A T A G T A	252	-
T A T G A A A T A T G T G A T A G T A A G A G A	253	-
A T T G T A A G A G T G A T T A T A G A T G A T	254	-
A G A G T A A G A A T G A A A G A G A T A A T A	255	-
T A A G T A A G T A G A T G T T A A A G A G A T	256	-
A A A T A G A A A G A A T T G T A G A G T A G T	257	-
A T A G A T T T T A A G T G A A G A G A G T T A T	258	42
G A A T G T T T G T A A A T G T A T A G A T A G	259	43
A A A T A G A A T G A G T A G T G A A A T A T G	260	-
T T G A A A T T G T A G A G A A A G T A A A G	261	-
T A G T A A A T T G A G A G T A G T T G A A T T	262	-
T G T A A A G T G T T T A T A G T G T G T A A T	263	-
A T A T G A T T T T G A G A T G A G A A T G T A A	264	-
A A T A T T G A T A T G T G T T G T G A A G T A	265	-
A G T G A G A T T A T G A G T A T T G A T T T A	266	44
T T G T A T T T A G A T A G T G A G A T T A T G	267	-
A T A G A A A T G A A A G A T A G A T A G A A G	268	-
G A T T G T A T A T G T A A A G T A G T T T A G	269	-
T A T G A A T G T T A T T G T G T T G A T T	270	45
G A T A T T A G T A G A G T A A G T A T A T T G	271	-
T G A G A T G A A T T T G T G T T A T G A T A T	272	-
T A T G A A T G A A G T A A A G A G A T G T A A	273	-
G A G T G A A T T T G T T G T A A T T T G T T T	274	-
A G A A A T T G T A G A G T T A A T T G T G T A	275	-
G T G T T A A T G A A A G T T G T G A A T A A T	276	-
T G T G A T T T G T T A A G A A G A T T A A T G	277	-
A G T A G T A T T G T A A A G T A T A A A G A G	278	-
T G A T T G T T G T A T A G T T A T T G T G T A	279	-
G A T T G T A G T T T A A A T G T T A A G A A T G	280	-
A T G A A A T A A G A A A T T G A G T A G A G A	281	-
T A T G A T G A T A T T T G T T G T A T G T G T	282	-
T T T A G A G T T T G A T T A G T A T G T T T G	283	-
A A T A A G A G A T T T G T G A T G A G A A A T A	284	-
A A T G A A T A G A A T A G A G A A T G T A G A	285	-
G T A G T A G T A A T T T G A A T G T T T G A A	286	47
A G T G A G T A A T T G A T T G A T T G T T A A	287	-
G A A T A A T G T T T A G T G T G T T T G A A A	288	-
A T A T G A A A G T A G A G A A A G T G T T A T	289	-
T G A G T T A T T G T A T T T A G T T T G A A G	290	-

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Sequence	SEQ ID NO:	No. in Ex 1
T A G T T G A G T T T A A A G T T G A A A G A A	291	-
T A A A G A G T G A T G T A A A T A G A A G T T	292	-
T G T A G T G T T T A G A G T A A G T T A T T A	293	-
A G A G A T T A A T G T G T T G A A A G A T T A	294	-
G T A A T A A G T T G T G A A A G A A G A T T A	295	-
G A G A T G T T A T A G A T A A T G A A A G A A	296	-
T T T A G T T G A T T G T T G A A A T A G A G T A	297	-
A T T A T T G A A A G T A G A T G T T A G A T G	298	-
T T T A T G T G T G A T T G A G T G T T T A A T	299	-
T A T T T A G T T A G A T A G A T A G A G A G T	300	-
A T G T G T T T A T G T G A A A G A T T T G T A	301	-
A T A G T A A T T A G A A G A G A A G A A T G T	302	-
T A T G A G T G A T T A G A A A T T G T A T T T G	303	-
T T A A T G T A T T G T T T A A A G A G T G T G	304	-
A T A G A G A A T T A A G A A T T G T T T G A G	305	-
G T T A T A A G T A G A A A T G T A T A G A A G	306	-
A G T A A T T A G T T T G A A A T G T G T A G T	307	-
G A A A G A T T A T G A T T G T A A A G T G A T	308	-
G T A A G A T T A G A A G T T A A T G A A G A A	309	48
G A G A A T G T T G A A T A A G A A G T A A T T	310	-
T T A A G A G T G T T T G A A T A G T G T T T A	311	-
A T A A A G A A A G A G T A T G A G A T T A T G	312	-
A G T T A T T G A T T G A A G A T G A G A A A T	313	-
G T T T G T G T T T G T A T A A G T T G T T A A	314	50
T T G T A T G T G A G T T T A G A T T A A T G A	315	-
T A G T T A A A G T A T A G T T G T T T G A G T	316	-
A A A T T T G T G T T G A G A T T T G T A T A G	317	-
T A T T A G T G T T A T G A T A A A G A G A A G	318	-
T A T A A G A A G T A A T T T G A G A A G A G T	319	-
T A A G T T G A G A T G T T T G T T G A T A A	320	-
G T G T A G A T T T A T G A A T T G A G T A A T	321	-
T A T A G A G A A G T G T T T A G T T G T A T A	322	-
A T A A A G A A G A A T A G T T G T T G T G T A	323	-
A G A T T G A A A T A G A T T A G A A A G T T G	324	-
G T T G T T A T A A G A A A T A G T T T G T T G	325	-
A G A A A T A G A G T A A G A G T G T T T A A A	326	-
A G A G A T A G T A G T A A A T A G T T A T T G	327	-
A A A T G A T T G T G T A A G T T A T G T A T G	328	-
A A G A A G T A A G A G A G A A A T T T G A A T	329	-
G T G T G T A T T T A G T T G A T A A T T G A T	330	-
A T T G T T G T T G T T G A G A A A T G T A T T	331	-
A G A T A A G T T A A A G T A A A G A G A A T G	332	-
T A G T T G A A G T T A G T T T A A G T G T T A	333	-
A G T A A G A A T G T A A A T A T G A T G A T A G	334	-
A T G A G A T T G A A A G A T T T A T G A A T G	335	-
T G A T T G A A T T A G A G A G A A T G T A T A	336	-
A G T T A G T A A G A G A A T A T A G T G A A T	337	-
A T T A A G A T T G T A T A G T T A G T G A T G	338	-
G A G A T A A A G A A T T G A A A T A G A A G A	339	-
A G A G T A A A T G T T A A G A A A G A A G T T	340	-
A A A G T T T G T T A T G T G T G A A G A A T T	341	-
A T T G T T G T T T A A G A A A T A T G A T G A G	342	-
T A T T G A A A T G A G A T G T A T G T A G T T	343	-
A T T T G T G T G A T G T T T G A A A T A T G A	344	-
T A A G A T A A T A G T G A G A G A A A T T G A	345	-
A T T T A T G A T T A G T G T A A G T G T T G T	346	-
G A T T A A G A A T A A A G T G T G A A G A A T	347	-

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Sequence	SEQ ID NO:	No. in Ex 1
G T A A T T G A T G A A G A G T T A G T T T A T	348	-
T G T G T T A T G T T A T A A G A A G T G A T A	349	-
A G A G A A A T T G A A T T T A G A A A T G T G	350	-
T T A T T G A A T G T G A G A A A G T A T T T G	351	-
T G T T A A T G A G A A G A T A A T G A T A G T	352	-
G A A A G T A T T T G T T G A T T A T T G T T G	353	-
T A G T T T A T G T A G T T A A T T G T T G A G	354	-
G T T G A A A G A T A G T T T G A T A T G T A T	355	-
T T A G A A G A T A G A T T A T T G A G A A A G	356	-
A A T A A T G T T G T G A A A T A G A T G T G A	357	56
A G T A A G A A A G T T T A G T T T A G T T A G	358	-
T A G T T T A A T G A G A T G T T T G A T A T G	359	-
T T A A A G A T G T T A A A G A A T G A G T G A	360	-
A A A G T G T A T A T G T T A G A A A G T A	361	-
A T T A A G T T A T G T T T A T G T G T T G	362	-
T T T G A A G A A G T G T T T G T A T T A T G T	363	-
T G T T A A G A A G T T T A G T T A A A G T T G	364	-
T T T A A G T A T A A G A T T G T G T G A G A T	365	-
A G A T A T T T G A T A G A T A G A A G A A A G	366	-
A T T T A G A G T T G T A A G A A G A T A T T G	367	-
G A G A A A T T G T A A T T G T T A G A G T A T	368	-
G A A G T A T A T G T T A A G A T G T A A T A G	369	-
A A T A T T G A A G A T G T A G T G A G T T A T	370	-
G A G T T T A G A A A T G A T A A A G A A T T G	371	-
T A A G A A A T G A G T T A T A T G T T G A G A	372	60
T T G A T A T A A G A A G T T G T G A T A A G T	373	-
A A G T G T T T A A T G T A A G A G A A T G A A	374	61
G T T G T G A G A A T T A G A A A T A G T A T A	375	-
T T T A G T T T G A A A G T A T G T T T A T G A G A T	376	-
G T A A T T G A A A G T A T G A G T A G T A A T	377	-
T A G T T G A A T A A G A T T G A G A G A A A T	378	-
T T A A G T G A A G T G T T G T T T A T T G A A	379	-
A T T G A T T T G T T G A A A T A A G T G T T G	380	-
T G A A T T G T T G A T A A G T T A T G A A G A	381	-
G T T T G T T A T T G A G T A A G T T G A A T T	382	-
T G A T T T A G T A T G T A T T A G A G T T G A	383	-
T A A A T A G A G A T G A G A A T A A G A A A G	384	-
A G A A T G T T A T A T G T A G A G A A A T T G	385	-
A T T T A T G T A G T T G A G A G T G A T A A A	386	-
G T A A A G A T A G T T T G A G T A A T T T G A	387	-
G A A A T A G T A T A A T G T T A A G T G A G A	388	-
A T T G T A T A T T G T G T T G A A A G A A A G T	389	-
G A G T T A A G T G T A A A T G A A A T G T A A	390	-
A T A G A T T G T G T G A A A G A A A G A A T T	391	-
T T A A T A G A A G T T T G T A G T A T G A T G	392	-
T T G T A T G T G A G A A T A A A G T T T A G T	393	-
G T G A T T A G A T A T G A T G A T A T G A A T	394	-
T G A A G A A G A A T T T A G A T T T G T A A G	395	-
T G T A T G A T T A T T G A T T A G T G T G T T	396	-
T G T G A A A G A G A A T G A T A G A T A T T T	397	-
A A T T G A A A T G A G T G T T T A A G A A A	398	-
A T T A T A G A G T T A G T T T A G A A T G A G	399	-
A A A G A T A G A A A T T G A G T G T A T G A T	400	-
G T A G T T T G T T A A T G T T G T A T A A T G	401	-
A G A G A T A T T A G A A T G T A A G A A T A G	402	64
A G A A G T T T G A A A T A T G A T A G A A T G	403	-
T A G A A T G T A A A G T T T A G T A T A G A G	404	-

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Sequence	SEQ ID NO:	No. in Ex 1
AGTAGATGTATGTTAAATGTGAATAA	405	-
TGAAAAGTGAAAATATGAAAATGTTGT	406	-
ATAGTATATTGAGTTTGTATGAAAG	407	-
GAAAGAAAATGTTTGTAGAAAATAAGTA	408	-
AATGAGTATTTGAAAGAAAATGTATAG	409	-
GTGATAGAAATTTGTGTTTAAATGAAA	410	66
TGTAGTATGAAAGAAATAATGAAAATG	411	-
ATAGAAAGTTAAATGATAAATGTGTG	412	-
GTGATTGTAAAGTAAGTAAGATAAA	413	-
TATGTAGTTTGTGTGTTATTTGAAAGA	414	-
TGAGTAAGTTTGTATGTTTAAAGTA	415	67
TAAAATGTATGAGTGTGTAAAGAAA	416	-
GTAAGAGTATTTGAAAATTAGTAAGA	417	68
GTTTGAGTGTAAAGATTAATGTATAA	418	-
AGTATGAGTTATTTAGATAAAAGTGA	419	-
ATTTGTATATAGAGTTGTGTTGTAT	420	-
TAAATTAGTAGTGTGTTGAAAATTTG	421	-
TGTATTGAGGATTTGTATTTGTATTG	422	-
GTTATTAGAAAGAGATAAATTGAGTT	423	-
TTGAGTTGTGATTAAAGTAGTATAT	424	-
GATAGTATAAATGATTGAAAGTAATG	425	-
GTGAAAAGATATTTGAGAGATAAAT	426	-
AGTTATGATTTTGAAAGAAAATTTGTG	427	-
GTAAGTATTTTGAATTTGATGAGTT	428	-
TAAATAGTGTATATAAGTGAAAAGAGT	429	-
AAAATGAAATTTGATGTGTATATGAAG	430	-
AGAAAAGTGAGTTGTTTAAGTATTTTA	431	-
TTTATGTGTGAATTTGTGTATATAG	432	-
GTAATATGATGATAAATGTAAAGAG	433	-
GAGAAATTTGTTTAAAGATAGTTGTA	434	-
GAAATTTGTTTAAAGAAATGAGTTTGTAT	435	-
ATAGTGATGATTAAAGAGAAATTTTG	436	-
ATAGATGTTTATAGTTTGAGATTATTTG	437	-
AAGAGTGTAATAATAGAAAAGTGATAT	438	-
TGTGTATTTGATTGTGTGAGATAAAT	439	-
TAGTATAGTGAGAAAGAGTTAAAT	440	-
AAAGATAAAGAAAGAGATGATGTTT	441	-
GAAAGTTATTTGAAAATAGAGAAAGTAT	442	-
ATGTATGTATATAGAAAGAGTAATAATG	443	-
GATGTTTGTAAAGATTTGAAAATTTGA	444	-
AATTTTAGAGAGGATTTTGTGTTGTA	445	-
AATTTGTTTTGAAGAAAGTAAGTG	446	-
AAAGAGTAGTGTATTTGTTAGATA	447	-
GATATGTTGATATGTTGTTGATAT	448	-
GTAGAAATTTGTGAGTATTTGTAA	449	-
ATGAAATTTAGTTAGTGTAAAGAAAG	450	-
ATGATAAGAAATGTTGATGAAGTA	451	-
TTGATGATGAAGATAAATGTAGATA	452	-
AGATGATATGATATAGATTAGATG	453	-
TTGAAAAGTTAGAAAGATAGATGTT	454	-
GTTTAAATGTAGTTAGAAAAGTAAG	455	-
GAGATTTTAAAGTTTGAAGTAATA	456	-
TTTGTATAGTAGTTGTATTAAGAGA	457	-
TATGAGAAATAGTTTGTATAGTGAAT	458	-
TTGAAAAGTTTAAAGAAAGAGATAAG	459	-
AAGTGAGTTTGAAAATGAAAATATGTT	460	-
GTTAGAAAATGAAAATGAGTAGTTAT	461	-

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Table I.

Sequence	SEQ ID NO:	No. in Ex 1
T A A G T A T T G T A T T T G T G T G T G T A T	462	-
T G T A T T A G T A A A G A A G A G A A T A	463	-
G A G A A G A G A A A T A A G T T G A A A T A A	464	-
G T A A A G T A G A A A T A G A A T T G A G T T	465	-
G T G T G T T A T T T G T T T G T A A A G T A T	466	69
T T T G A T G T A T G A A T A T A G T A T G A G	467	-
A A G A T T G T G T G A A T A G T T G A A A T T	468	-
T A T A A A G T T T G A A G A T G A G T G A T A	469	-
A G A T A A A G A G A T T T A A G A T G T A T G	470	71
G A A G A A T T A A G T T G A G A A T T A A G A	471	-
T A G A G A A A T T T G A T A A A G A A A G A G	472	-
A A A G T T T A T G A A G T T A T T G A G T A G	473	-
A A A T A G T G T A A G T A A A G A G A T G A T	474	-
T A T G A T G A T T T A G T T A T A A G A G T G	475	-
T A G A T A A A T G T T A T G A T G A G T A A G	476	-
A G A T T G A T T G T G A T G A T T T G T A T A	477	-
T T A A G A A G A A T T G T A T A T G A G A G T	478	73
G T A G A A T G T T T A G A G T T G A A T A T A	479	-
G A G A A A T A G T A A G A A G T A A A T A G A	480	-
A T T G A A G T T G T T A T G T G A A G A T T T	481	-
T A A A T G T T G T G T A G A G T A A T T A G A	482	-
A A A T A A G A G T T T T G A G A A G T T G T T T	483	-
A G T T G T A A T A A G A A G T G A T T T A A G	484	-
G T T A G A A T G T A T A T A G A G T T A G A T	485	74
T T G A T A T T G A A A G A G A A A G T T A T G	486	-
T T A A A G A G A G A A A T G T T T G A T T A G	487	-
T G T G A A T T T G A G T A T T A G T A A G A A	488	-
T A A T T T G A A T G T G A A A G T T G T T A G	489	-
A T G T G T T T G A A A G A T G A T G A T T T A	490	-
A A G T T A T G T T G A T A T T G A G T G A A A	491	-
T A G A T A A A G A A G A T A G A G A T T T A G	492	-
G A T G A A T G T A G A T A T A T G T A A T G A	493	-
G A A G A A T A G T T T A T G T A A A T G A T G	494	-
G T A G T A T A T A G T T A A A G A T G A G T T	495	-
G T T A T T T G T G T A T G A T T A T G A T T G	496	-
A G A G A T T A G A A A T T G A G A G A A T T A	497	-
G T A T G A T A G A G T T T A T A G T G A T A A	498	-
G T T A G A A A G A A T G A A A T T G A A G T A	499	-
A A G A A T G A G A A T A T A G A G A T G A A T	500	-
A A A G A G A A T A G T G T T T A A G A A G A T	501	-
G A T G T G T T A T T G A T A G A A A T T A G A	502	-
T A G A G T T A T A G A G A T A T T G T A T G A	503	-
G A G A G T T G A A A T A A G T T A A A G A T A T	504	-
A G A T A T G A A A T A G A T T G T T A G A G A	505	-
G A G T G A A T A G A A A G A T A T G T T A A T	506	-
A A A G A G A T A T T G A A G A G A A T A A A G	507	-
G T T A T A G A A T A A G T T G T A A A G T G T	508	-
T G A T A G T A T G A T A A T G T G T T T A T G	509	-
T T T G T T G T T A A G T A T G T G A T T T A G	510	77
T A A A G T G T T G T G T T A A A G A T T A A G	511	-
T G T G T T T G A T T G A T T A A T G T T A T G	512	-
A T T A A T G A A T G A G T G T G T A A T G T	513	-
T A G A T G T T T G T G A G T T T G A T A T T A	514	-
G A A T G A A T A G T A A T A G A T G A T T T G	515	-
A A T A G T G T G T T G T T A T A T G A T T A G	516	-
T A G A T T A G A A G A T G T T G T G T A T T A	517	-
A A T G T G T G T G T T A A A T G A A T T T G T	518	-

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Sequence	SEQ ID NO:	No. in Ex 1
G A A T T A A G T A T A T G A G T G T A G A A A	519	-
T T A T T G T G T G T A A G T A G T G T A A A T	520	-
G T A G T A A A G A G A A T T G T T T A G T A T	521	80
A A G T T T G T A A G A A G T A G T T G A A T A	522	-
A G T T A T A G T A T A G T A G T A T A G A G A	523	-
G A A A G A A A T G T G T A T A G T T T A A T G	524	-
T T G T G A G T A A T G A A T G A T G T A T T A	525	-
G T A G A G T T G T A A A T A G A G A A T A A A	526	-
A T T A A A T G T A G A T T G T A A G A G A T A G	527	-
T T A G T G T G T T T G T A G A T A G A A T T A	528	-
A G A G A G T T T G T G T A T A T G T A T A A A	529	81
T T A A G T T T A G T G A G A T T T G T T A A G	530	-
A T G A A G T T T A T T G A A T A G T A G T G A	531	-
A T A T T T G T G T T T G T A T G T T T G T G A A	532	-
A A A G T G T T T A T A G A A G A T T T G A T G	533	-
A A G A G A T A T G A T T T G T T A G T T G T A	534	-
A A G A A G A A A T G A G T G A T A A T G T A A	535	-
T A G T G T T T G A T A T G T T A A G A A G T T	536	-
G T A G A A A G T G A T A G A T T A G T A A T A	537	-
G A T A A A T G T T A A G T T A G T A T G A T G	538	-
A G A T T A G A A G A A A T T G T T T A G A A T G	539	-
A T A T T T G A G A A G T G T G A A A T G A A T	540	-
T G A G T A A A T A G T T T A T G A G T A G T A	541	-
T T A G A G A G T A G A T A A A G A T T T G A T	542	-
A T T G T T T A A G T T G T T G A T A A G A T G	543	-
G T T G T A A A G T T A A A G T G T G A A T T T	544	-
A T A G A T T G T G T G T T T G T T A T A G T A	545	-
G T A A G T T A T T G A G A A T G A T A A T A G	546	-
T A G A T T A G T T G A T A A G T G T G T A A T	547	83
A A A T G T A A A T G A A G A G T G T T T G T T	548	-
G A T A G A A G A A A T G T A T A T A G T G A T	549	-
T A T A G A G T G T A T G T T A T G A T A A A G	550	-
T A T G A A G T G A T A A G A T G A A G A A T T	551	-
T G T T G A G A A T A G T A A G A G A A T T T A	552	-
T A G A T A A T G T G A A G T A A T A A G T G A	553	84
G T A T T A T G A T T G A T A G T A G T A A G T A	554	-
A G A T A T G A T T T A G T A T T G A A T G T G	555	-
A A T T A A G T T T G T A G A G T G A T T T T G A	556	-
A A G A A A T A G A T G T A G T A A G A T G T T	557	-
T T G A G A A G T T G T T G T A A T A A G A A T	558	-
A G T G T G A A A T A G T G A A A G T T T A A A	559	-
T T T A T G T A G T A G A T T T A T G T G A A G	560	-
A T T A A T G A G A A A T T A G T G T G T T A G	561	-
A T G T T A A T A G T G A T A G T A A A G T G A	562	-
T A T G T T G A T A A A T G A T T A T G A G T G	563	-
T T A T T A G A G T T G T G T G T G A T A T A T	564	-
T G T T G T T A T G A T T G A G T T A G A A T A	565	-
A A T T T G A G T T A A G A A G A A G T G T A A	566	-
A A A G A T A A A G T T A A G T G T T T G T A G	567	88
T G T T G A G A T G A T A T T G T A T A A G T T	568	-
T A A A T A G T G A A T G A G T T A T A G A G T	569	-
A T A G A T G T T A T G A T A G T T A G T T A G	570	-
G T T A A G T G A A G A T A T G T A T T G T T A	571	-
T A A G A A A G T A A A G T T T G T A G A T G T	572	-
A A G A G A A A G T T T G A T T G A A T A A A G	573	-
A T A T T A G A T G T G A G T T A T A T G T G T	574	-
A G T T T G A G T T T A G T A T T G T G A A T A	575	-



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Sequence	SEQ ID NO:	No. in Ex 1
A T G T T A A A T G A G A G A T T G T G T A T A	576	-
T A A A T G T T G T G A T T A T T G T G A G A T	577	-
T A A G A A T T G A A G T A A G A G T T A T T G	578	-
A G A G A T A G A A T T A A G T T T G T T G A T	579	-
G A A G A A T G T T A A G A A A T A T G T A A G	580	-
T A T T T G T G A T T A A G A A G T T G A G A A	581	-
A G T T A G A A T T T G T G T A G T A G A A T T	582	-
A A G T T T A T T G T T G A T G T T G T A T T G	583	-
G A A T G A G T T T T A A G A G T T T A T A G T A	584	-
A G T G A A G A T T G T A T G T A G T A T A A A	585	-
A G T T G A A A T G A G T A T T A A G T A A T G	586	-
A T G T G T T A T T T T G A G A T G A G T A A T T	587	-
A A A T A G T G T T G T T G A A G T T G T T A T	588	-
G T A G A G A A A G A T A T A T G T A G T T T A	589	-
G A G A G T A T T T T G A T G A A T G A T T A T A	590	-
G A G T A T A A G T T T A G T G T A T A T T G A	591	-
A T A A T G T G A T T A T T G A T T G A G A G A	592	-
T T A G T T G T T A T G T G A G A G T A A T A A	593	-
A A A T G A G T A T A T T G A A T T G T G A T G	594	-
A A T T A G A A G T A A G T A G A G T T T A A G	595	3
T G T A A A G T T T A A A G T A A G A A A T G T G	596	5
G A A A T G A T A A G T T G A T A T A A G A A G	597	-
A A T G A G T A G T T T G T A T T T G A G T T T	598	-
A G T G A A T G T A A G A T T A T G T A T T T G	599	6
G T A A T T G A A T T G A A A G A T A A G T G T	600	8
T A T G T T T A A G T A G T G A A A T A G A G T	601	-
G T A T T T G A A A T T G A A T T A G A A G T A G	602	-
A A T A T G T A A T G T A G T T G A A A G T G A	603	-
T G A A T A T T G A G A A T T A T G A G A G T T	604	-
T A G T G T A A A T G A T G A A G A A A G T A T	605	-
G T A T G T A A A G A A A T T T G A T G T A	606	-
A A T T G T T T G A A A G T T T G T T G A G A A	607	-
A A T T G T T T G A G T A G T A T T A G T A G T	608	-
T A A T T G A G T T T G A A T A A G A G A G T T	609	-
T G T T G A T T G T A A G T G T T T A T T G T T	610	-
G A A A T T T G T G A G T A T G T A T T T G A A	611	-
T A A G A A T G A A T G T G A A G T G A A T A T	612	-
T A A T G T G A A G T T T G T G A A A G A T A T	613	-
T T G T A T A T G A A A G T A A G A A G A A G T	614	-
T A G A G A G A A G A A G A A A T A A G A A T A	615	-
A T T T G A A A T G T T A A T G A G A G A G A T	616	-
T T G T G T G T A T A T A G T A T T A G A A T G	617	-
A T T G T T A G T A T T G A T G T G A A G T T A	618	-
T G T T T G T A T T T T G A A T G A A A T G A A G	619	-
T G T T A G A A T T G T G T T A A A T G T A G T T	620	-
T A T A G A G T A T T G T A T A G A G A G A A A	621	-
A A A T A G T A A G A A T G T A G T T G T T G A	622	-
T G A G T G T G A T T T A T G A T T A A G T T A	623	-
A G A A T T T G T T G T A G T G T T A T G A T T	624	-
G A T T G A A G A A A G A A A T A G T T T G A A	625	-
G A T A A T A G A G A A T A G T A G A G T T A A	626	-
G A T T T G A A A T T T G T A G T T A T A G T G A	627	-
G A T T T G A A G A A G A T G A A T A A T G T A G	628	-
T T T G A G A G A A A G T A G A A T A A G A T A	629	-
G A T T A A G A G T A A A T G A G T A T A A G A	630	-
T T T G A T A G A A T T G A A A T T T G A G A G	631	-
T G A A G A A G A G T G T T A T A A G A T T T A	632	-

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Sequence	SEQ ID NO:	No. in Ex 1
G T G A A A T G A T T T A G A G T A A T A A G T	633	-
A A A T A A G A A T A G A G A G A G A A A G T T	634	9
G T T G T A A A G T A A T A G A G A A A T T A G	635	-
A G T G A T T T A G A T T A T G T G A T G A T T	636	-
A G A G T A T A G T T T A G A T T T A T G T A G	637	-
A T G A T T A G A T A G T G A A A T T G T T A G	638	-
A T G A A A T G T A T T A G T T T A G A G T T G	639	-
A T A T T G A G T G A G A G T T A T T G T T A A	640	-
A G A T G T G T A T T G A A T T A A G A A G T T	641	-
T A A T G T G T T G A T A G A A T A G A G A T A	642	-
A A A T T A G T T G A A A G T A T G A G A A A G	643	11
T T T A G A G T T G A A G A A A T G T T A A T G	644	-
G A T T G T T G A T T A T T G A T G A A T T T G	645	-
T G T T G T T G T T G A A T T G A A G A A T T A	646	-
A T T A A G T A A G A A T T G A G A G T T T G A	647	12
G T A T G T T G T A A T G T A T T A A G A A A G	648	15
T A G T T G T G A T T T A T G T A A T G A T T G	649	-
T G A T A A T G A A A G T T T A T A G A G A G A	650	-
G T A A G A T T G T T T G T A T G A T A A G A T	651	-
T T G A A T T A A G A G T A A G A T G T T T A G	652	-
A A G T G T T T G T T T A G A G T A A A G A T A	653	-
A G A G A G A T A A A G T A T A G A A G T T A A	654	-
A T T A T G A A T A G T T A G A A A G A G A G T	655	-
T T G T T G A T A T T A G A G A A T G T G T T T	656	-
T T T A T T G A G A G T T T G T T A T T T G T G	657	-
A G T G T T A A G A A G T T G A T T A T T G A T	658	-
G A G A A A T G A T T G A A T G T T G A T A A T	659	-
G A T A A G T A T T A G T A T G A G T G T A A T	660	-
T T T G A T T T A A A G A G T G T T G A A T G T A	661	16
A A G T T A G A A T A G A G T A G A A A G A	662	-
G T A A A G T A T G A A T A T G T G A A A T G T	663	-
T A A T A A G T G T G T T G T G A A A T G T A A T	664	-
A A A G A T T T A G A G T A G A A A G A G A A T	665	-
T T A G T T T G A G T T G A A A T A G T A A A G	666	-
T A A T A G T A T G A G T A A G A T T G A A A G	667	-
G A A G A T T A G A T T G A T G T T A G T T A A	668	-
T A A A G A G A G A A G T T A G T A A T A G A A	669	-
T A A G T A T G A G A A A T G A T G T G T T A T	670	-
G A G T T T G T T T G T T A G T T A T T G A T A	671	-
A A G T A A A G A A A T G T T A A G A G T A G T	672	-
A T G A G A A T T G T T G T T G A A A T G T A A	673	-
T T A G A T T A G A G T A G T A G A A G A A T A	674	-
T A G T G A T G A A G A A G T T A G A A A T T A	675	-
T A A T G T A G T A A T G T G A T G A T A A G T	676	-
T T G A G A A A G A A T A A G T A G T G T A A A	677	-
T A A T G A G T G A G A T T A T A G A T T G T T	678	-
G T A T A A G A A A T G T G T G T T T G A T T A	679	-
G T G A A T G T G T T A A T G A A A G A T A T A T	680	-
G A A A G T T A T T A G T A G T T A A A G A T G	681	-
T A G A A T T G T G T T T G A T A A G T G A T A	682	-
T G A T T T A G A T T G A G A G T T A A A T G A	683	-
A T T A T T G A G T T T G A A T G T T G A T A G	684	-
A T A G T A G T T A T G T T T G A T T T A G T G	685	-
A T A G A A G A A G A A T A A A G T T A G A G A	686	-
G A T G T T G A A A G T A A T G A A T T T G T A	687	-
G A G A T T G A T A G T A G A A A T G A T A A A	688	-
T G A G A G A A T A A A G T A T G A A T T T G A	689	-

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Sequence	SEQ ID NO:	No. in Ex 1
T A T A A A G A T G A T G T G A A T T A G T A G	690	-
T T A T G T A A G A A T G T T T G A G A G A A A	691	-
A G T A A A T G A T G A A T G A T A T G A T G A	692	-
G A A A T T T G T G T T A A A G T T G A A T G A	693	-
G A T G A A T G A T T G T G T T T A A G T A T A	694	-
G A A A T A A G T G A G A G T T A A T G A A A T	695	-
T G T T G A A A T A G T T A T T A G T T T G T G	696	-
T T T G A G A G T A T A T T G A T A T G A G A A	697	-
A T T G T G T G T A A A G T A A G A T T T A A G	698	-
T A T A G T T T G A A G T G T G A T G T A T T T	699	-
G T G A A G T T A T A G T G T A T A A A G A A T	700	-
G T A T G T T G A A T A G T A A A T A G A T T G	701	-
T T A G A A A G T G T G A T T T G T G T A T T T	702	-
T T T A G T A A T A T G T A A G A G A T G T G A	703	-
A G T A T G T A T A G A T G A T G T T T G T T T	704	-
A T T T A A G T A A A G T A A G A G A T A A G	705	20
A T T T G T G T T G A A T T G T A A A G T G A A	706	-
A T G T T A T T A G A T T G T G A T G A A T G A	707	-
T A G T A G T A G A A T A T G A A A T T A G A G	708	-
T T T A A T G A G A A G A G T T A G A G T A T A	709	-
A A A G T T T A G T A G A G T G T A T G T A A A	710	-
A T A T A T G A T A G T A G A G T A G A T T A G	711	-
T G A G A A G A T T A A T T G T A T A G A T T G A	712	-
T A T A G A G A T G T T A T A T G A A G T T G T	713	-
A A A T T T G T T A A G T T G T T G T T G T T G	714	-
T T G T T T G A A G A T G A A A G T A G A A T T A	715	-
A A G A G A T A A G T A G T G T T T A T G T T T	716	-
A A T A A G A A G A A G T G A A A G A T T G A T	717	-
T A A G T T A A A G T T G A T G A T T G A T A G	718	-
A T A T A A G A T A A G A G T G T A A G T G A T	719	-
G T T A A A T G T T G T T G T T T A A G T G A T	720	-
G A G T T A A G T T A T T A G T T A A G A A G T	721	-
T A T T A G A G T T T T G A G A A T A A G T A G T	722	21
T A A T G T T G T T A T G T G T T A G A T G T T	723	-
G A A A G T T G A T A G A A T G T A A T G T T T	724	-
T G A T A G A T G A A T T G A T T G A T T A G T	725	-
A T G A T A G A G T A A A G A A T A A G T T G T	726	-
A G T A A G T G T T A G A T A G T A T T G A A T	727	27
A T G T A G A T T A A A G T A G T A T G T T	728	-
T T A T T G A T A A T G A G A G A G T T A A A G	729	-
A T T T G T T A T G A T A A A T G T G T A G T G	730	29
T T G A A G A A A T A A G A G T A A T A A G A G	731	-
T G T G T A A T A A G T A G T A A G A T T A G A	732	-
A T G A A A G T T A G A G T T T A T G A T A A G	733	37
A T T A G T T A A G A G A G T T T G T A G A T T	734	-
T G T A G T A T T G T A T G A T T A A A G T G T	735	-
A G T T G A T A A A G A A G A A G A G T A T A T	736	-
G T A A T G A G A T A A A G A G A G A T A A T T	737	-
T G T G T T G A A G A T A A A G T T T A T G A T	738	-
A A G A A G A G T A G T T A G A A T T G A T T A	739	-
G A A T G A A G A T G A A G T T T G T T A A T A	740	-
A A A T T G T T T G A G A T A A G A T A G T G A T	741	-
T G A T T G T T T A A T G A T G T G T G A T T A	742	-
A T G A A G T A T T G T T G A G T G A T T T A A	743	-
G T G T A A A T G T T T G A G A T G T A T A T T	744	46
A A T T G A T G A G T T T A A A G A G T T G A T	745	-
T T T G T G T A A T A T G A T T G A G A G T T T	746	-

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Sequence	SEQ ID NO:	No. in Ex 1
G T A G T A G A T G A T T A A G A A G A T A A A	747	-
T T T A A A T G T G A A A T T T G T T G T G A G T	748	-
G T A A A G A A T T A G A T A A A G A G T G A T	749	-
A A T A G T T A A G T T T A A G A G T T G T G T	750	-
G T G T G A T G T T T A T A G A T T T G T T A T	751	-
G T A T A G T G T G A T T A G A T T T G T A A A	752	49
G T T G T A A G A A A G A T A T G T A A G A A A	753	-
A T A T T A G A T T T G T A A A G A G A G T G A A	754	-
G A G T G A T A T T G A A A T T A G A T T G T A	755	-
T A A G A A G T T A A A G A A G A G A G T T T A	756	-
G A T G T T A G A T A A A G T T T A A G T A G T	757	-
G T G A T T G T A T G A G A A A T G T T A A A T	758	-
T G A T T A T T G T A A G A A A G A T T G A G A	759	-
A A G A A T T G T G T A A G T T T A T G A G T A	760	-
T T G T A T T T A G A A G A T T T G T A G A T G	761	-
T A T A T G T T T T G T G T A A G A A G A A A T G	762	-
G A T A A T G T G T G A A T T T G T G A A T A A	763	-
T T A G A A A T G T G A G A T T T A A G A G T T	764	-
A G T G T A G A A T T T G T A T T T A G T T G T	765	-
T A G T T A A G A T A G A G T A A A T G A T A G	766	-
G A A G T G A T A T T G T A A A T T G A T A A G	767	-
G T A A A T T G T G T T A G A T T T A A G A A G T	768	-
T G A T A T T T G T G A A T T G A T A G T A T G	769	-
A A G T A A A G A G A T A T A G T T A A G T T G	770	-
A T T A G T T A A G T T A T T T G T G A G T G A	771	-
A G A T G A A G T A G T T T A T G A A T T A G A	772	-
T G A G T T A G T T A A G T G A T A G T T A A A	773	-
T T A T T G T A G A T T T A G A G A A G A T G A	774	-
T A T T T G T G T T T G T T G A T T A G A T A G	775	-
G T A T A A T G T G T G T G A A A G T T A T A A	776	-
T A T A T G T T G A G T A T A A A G A G A G A A	777	-
T T A G T T A G T T T A A A G A T T G T G A G T	778	-
T T T A G A A T A A G T G A T G T G A T G A A A	779	-
A G A G T A A T G T G T A A A T A G T T A G A T	780	-
T G T G A T A A A G A G A A A T T A G T T G T T	781	-
G A A T T T A G T G A A T G T T T G A G A T T A	782	-
T G T G A T G T G T A A G T A T A T G A A A T T	783	-
T T G T G A A T G A T T A A T G A A T A G A A G	784	51
A A T G T T G T T T A G A T T G A G A A A G T T	785	-
A G A T T G T G T T A G T A T T A G T A T A A G	786	-
T T G A T G T A T T A G A A A G T T T A T G T G	787	-
T A T G A T T G T G T G T T A G A G A A T T T A	788	-
T A G T G T A G A T A T T T G A T A G T T A T G	789	52
A G T T T A A T G T G T T T A G T T G T T A T G	790	-
T G T G T A A A G T A G A A A G T A A A G A T T	791	-
G T T A T G A T A T A G T G A G T T G T T A T T	792	53
T T T G A T T G A A T G T T A A T A G T G T G T	793	-
A G A G T A T T A G T A G T T A T T G T A A G T	794	54
T A A G T A G A A A G A A G A A G A T A T T T G	795	-
A G A A A G A G A A T T A T G T A A T G A A A G	796	-
T T A G A T T T G T T A G T G T G A T T T A A G	797	-
G A T G A T T A A G A T A T A G A G A T A G T T	798	-
A T A T T T G A G T G A T T A A G A G T A A T G	799	-
T G T A T T G T G A G T T A A G T A T A A G T T	800	-
A A T T T A G T A G A A A G T G T T G T G T T T	801	-
G T T A G A A G A T T A A G T T G A A T A A T G	802	-
T A A A G T A T G T G A G A T G A T T T A T G T	803	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
TGAAAATGATTAAAGATGAAAGATGA	804	-
TTATTAGATGTTTGAGTGTTTGT	805	-
TAGTGTTTAAAGAGTAGTATATGA	806	-
AGTTATAGTAAATGATGTTGATG	807	-
TTAAGAGAGAAATAAGTGTTTGT	808	-
GATATTGAAATGTTGTAATAATGATGA	809	-
ATGATGAAATTAAAGAAAGAGAGA	810	-
GAAATAGTTTGTATTGTTGTTTA	811	-
AGTTGTTTAGATTTTGATTGTAAG	812	-
GTATGAGATTTTGATATAAGATTAG	813	-
TTTATAGTGAGGTATAGTGATT	814	-
TATATAGTGAAAGATATAAGTGTTTG	815	-
ATTGATAGATGATAGTAAATTGAGT	816	-
TGATAGATGTTGAAGAAATTTGATT	817	-
GAAAGATATTGAAAGAAATTTGATGT	818	55
GATGTTTAGTGTTAGATATAGATT	819	-
GAAATATTGAGTTATAAGTAGTAGT	820	-
AGTGAGTAAGTAATAAGAAAGATT	821	-
GTAGAAATAAGTAATTTGTGAGATA	822	-
GAGTTATTTTGAGATTTTAGATGTT	823	-
GAAATGATGATTGAAATTTAGAGAT	824	-
AAATAGTTGTGAGAAATAGTTAAGTA	825	-
ATGTTGTTAAGTTGTAGAAAGATAA	826	-
ATAATGAGTTAATAGTGTAAGAAAG	827	-
ATAAGAGATGTTTAAAGTTAGAAAG	828	-
TGTTAGTGTTTAGAAATAATGAAAGA	829	-
TTTAGAAGATTGTTTAGATAAAGTTG	830	-
GTGTAATGTATAAAGATAGTTTAAGT	831	-
TATTAGAGAGAAATTTGTAGAGATT	832	57
TAGTGAGATAAAGTAAGTTTATG	833	-
TTGTGAAAGTTAAGTTAAGTTAGTT	834	-
AAAGTGTAAGTTGAAGAAATATTGA	835	-
GAAATAGAGTGTTATTTTGAAATAGA	836	-
TATAAGAGAGAGATAAGTAATAAG	837	-
TGAGTGAAATTTGATAGAGTAATAAT	838	-
GATGAAATAAGTTTAAAGTGAGAAAT	839	-
GTGTGATATGTTTATTGATTAAAGT	840	-
TAAAGTGAGTGTTAAATGATAAATGA	841	-
GTAGAGTTTGTATTGAAAGAAATAT	842	-
GAAATATTGTTATGTTTGTATTGAG	843	-
GTGTAAATAAGATGTTATTGTTGTT	844	-
TAAATTTGATTGTTGAGTTTGAAGAA	845	-
TGAGATAGTTTATAGTTAAGTTTAG	846	-
AGTTTGTGTTAAGATTATGTAGAAAG	847	-
GAAATGTTGTAAGAAATAGAGATAAA	848	-
GTATTATGAAAGAAAGTTGTTGTT	849	-
GTGTTATAGAAAGTTAAATGTTAAG	850	58
TTAAGAGTAGTGAAATATGATAGTA	851	-
AATGTTATATAAGATGAGAGTTTAGT	852	-
ATATATAAGATTTTGATGTTAGTAGT	853	-
TATGTTTGTGTTGTTTAAAGTTTGA	854	-
GATAGTTTATAGTATAGAGATAAAG	855	-
GTTGAATATAGAGATAGATAAATAG	856	-
AGAGAAAGATTTTAGTAAGAAATGATA	857	-
TGAAATGAGAAAGATATTGAGTATT	858	-
TGAAGATTATAGTAGTTGTATAGAA	859	-
GATTAGTAGTATTGAAGATTATGT	860	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
TGAAAATGTGTATTTGTATGTTTAG	861	59
ATTAAAGTTGATATGAAAGAGTG	862	-
AATGTAGAGATTGTAGTGAAATATT	863	62
TTATTTGTGTGAGTGTAAATGTGAT	864	-
ATGTTAATTGTGAAATAATGTATGTG	865	63
GATTTGTATAGAGATTAGTAAGTA	866	-
AATATTGTGTGTTTAGAGAAAGAAAG	867	-
ATGATGATGTATTTGTATTAAGAGTA	868	-
AATGTATTTGTGTGATTTGTGTAATA	869	-
AGTGTATATGAAGAAATAGTAAGAAAT	870	-
GTTATGTAGAGAGATGAAGAAATTA	871	65
GTTTGTATTTAGATAAATGAGTTGT	872	-
TGATTTATGAGATTAAAGAGAAAGA	873	-
TTTGTGTGTATTTGTAAATTGAGAT	874	70
GATGTGTGATATGATTTAAAGAAAT	875	-
AGATTATAGATTGTAGAGAAAGT	876	-
GAAAGAGTATGTAAATAGTATTGTAT	877	-
TTTGTAAATGTGTGTGTGAAGTTTAAGA	878	-
AGTAAATAGTAGTATGAATAAGAG	879	-
GAAATGTTGAATTGAAATATGAGTT	880	-
AGTAGTTAATTGATAGTAAAGTTTG	881	-
AGTGTAAAGAAATGAATAAGAAATAG	882	-
TGTTAGATTATTTGTGAAATGTGAA	883	-
TGTATGTTGTGAGTTTGAATTGTAT	884	-
TGAGTGAAATTAGTTATGTTGTAT	885	-
GAAAGAAAGAAATGAGAAAGATTAT	886	-
TTAAGTAAGTTGTGTGTGATATTAG	887	-
ATGATGTGTTTGTATTTGAATTGAA	888	72
AAGTAAGTGAAATTTGTTTGA	889	-
ATGAAGTGTAAGTTTGAAAGAA	890	-
AGAGATAAGATAATTGTATAGTA	891	-
TTTATGAGATAGATGAATAAGTG	892	-
AGAAATTAGTAGTAATTGTTGTG	893	-
GATTTGAGATTGAAATGAGAAATATA	894	-
GATTAGAAAGATGAATAAAGATGA	895	-
TAGATAGAAAGTATATGTTGTAGT	896	-
GAAAGATAGTAAAGTAAAGTAAAGTT	897	-
AAATGTGTGTGTAGTAGTTGTAA	898	75
TTGTTGAAGTAAAGAGATGAATA	899	-
TATTTGAGAGAAAGAAAGAGTTTA	900	-
TATTTAGTGATGAATTGTGATGT	901	-
TTATAGTGATGATGATAAGTTGAT	902	-
TAAAGATAAATTGTAGAAAGTAGTG	903	-
GTTTAGTATTTGATATTGTGTGTA	904	-
TTGTTGTGAATAAGATTGAATAAT	905	-
AAAGAAAGTATAAAGTGAGATAGA	906	-
TATTTGTAAAGAAAGTGATATTG	907	-
TAGAAAGATGAATAATTGTGTTTGT	908	-
ATAATAGTAAAGTGAAATGATGAGAT	909	-
AATGTGAATAAAGATAAAGTGTTA	910	-
ATTGAAGATAAAGATGTTGTATTAG	911	-
TGAAATTAGAAGTGAGATTATAGTA	912	76
AGTTATTGTGAAGAGTTTATGAT	913	-
AAATAGTAGTGATAGAGAAAGATT	914	-
AGTGTATGAAGTGTAATAAGATT	915	-
TGATTAAGATTGTGTAGTGTTATA	916	-
AGTTTATGATATTTGTAGATGAGT	917	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
T A T G T G T A T G A A G A T T A T A G T T A G	918	78
G A A A T T G T T G T A T A G A G T G A T A T A	919	-
T A G A A A T A G T T T A A G T A T A G T G T G	920	-
T G A T T T A G A T G T T T A T T G T G A G A A	921	-
A A G T T G A T A T T T G T T G T T A G A T G A	922	-
T G A T G T G A T A A T G A G A A T A A A G A A	923	79
A A A G T T T A G T T T G T A T T A G T A G A G	924	-
A G T T T G A T G T G A T A G T A A A T A G A A	925	-
A A G T G T T A T T G A A T G T G A T G T T A T	926	-
A A A T T G A A G T G T G A T A A T G T T T G T	927	-
G T T T A G T G A T T A A A G A T A G A T T A G	928	82
A T A A G T G T A T A A G A G A A G T G T T A A	929	-
A T G A A T T T G T T T G T G A T G A A G T T A	930	-
A A A G A A T T G A G A A A T G A A A G T T A G	931	-
A G T G T A A G A G T A T A A A G T A T T T G A	932	-
G A A T T A A G A T T G T T A T A T G T G A G T	933	-
T A T G A A A G T G T T G T T T A A G T A A G A	934	-
T A A A G T A A A T G T T A T G T G A G A G A A	935	-
A A A G A T A T T G A T T G A G A T A G A G T T	936	-
A A G T G A T A T G A A T A T G T G A G A A A T	937	-
A A A T A G A G T T T G T T A A T G T A A G T G	938	-
G A T T T A G A T G A G T T A A G A A T T T A G	939	-
T T G T A A A T G A G T G T G A A T A T T G T A	940	-
A G T A G T G T A T T T G A G A T A A T A G A A	941	-
T G A G T T A A A G A G T T G T T G A T A T T T	942	-
A A A G A G T G T A T T A G A A A T A G T T T G	943	-
G T T T A G T T A T T T G A T G A G A T A A T G	944	-
A A G T G T A A A T G A A T A A A G A G T T G T	945	-
A A T A A A G T G A G T A G A A G T G T A A T T	946	-
T A T T G A G T T T G T G T A A A G A A G A T A	947	-
T T T A T A G T T T G T T G T G T T G A A A G T T	948	-
A T G A A A T A T G A T T G T G T T T G T T G T	949	-
A A A G A G A T G T A A A G T G A G T T A T T A	950	-
T T G A A G A A A G T T A G A T G A T G A A T T	951	-
A T G T T A T T T T G T T T A G T T T G T G T G A	952	-
A A A T A T G A A T T T G A A G A G A A G T G A	953	-
G A T T A G A T A T A G A A T A T T G A A G A G	954	-
T T A G A A T A A G A G A A A T G T A T G T G T	955	-
T T T A T G A A A G A G A A G T G T A T T A T G	956	-
G T A A G T A T T A A G T G T G A T T T A G T A	957	-
A T A A A G A G A A G T A A A G A G T A A A G T	958	-
A T T G T T A A T T G A A G T G T A T G A A A G	959	-
T A T A T A G T T G A G T T G A G T A A G A T T	960	-
T A G A T G A G A T A T A T G A A A G A T A G T	961	-
A T A A G A A G A T G A T T T G T G T A A A T G	962	-
T T A G T A A T A A G A A A G A T G A A G A G A	963	-
G A T T T G T G A G T A A A G T A A A T A G A A	964	-
A A A T A G A T G T A G A A T T T G T G T G T T	965	-
G A A A T T A G T G T T T G T G T G T A T T A T	966	-
A T T T G A G T A T G A T A G A A G A T T G T T	967	-
A T A G A G T T G A A G T A T G T A A A G T T T	968	-
T A A T T T T G T G A A T G T T G T T A T T G T G	969	-
T T A G T T T A T G A G A G T G A G A T T T A A	970	-
G T T G T T A G A G T G T T T A T G A A A T T T	971	-
T T T A T T G T G A T G T G A A A T A A G A G A	972	-
G T A A G T A A T A T G A T A G T G A T T A A G	973	-
T G A G A T G A T G T A T A T G T A G T A A T A	974	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
A A T T G A G A A A G A G A T A A A T G A T A G	975	85
T T T G A A G T G A T G T T A G A A T G T T T A	976	-
A G T T G T T G T G T A A T T G T T A G T A A A	977	-
A T A G T G A G A A G T G A T A A G A T A T T T	978	-
G T G T G A T A A G T A A T T G A G T T A A A T	979	-
T A G T T A T T G T T T G T G A A T T T G A G A	980	-
A T A G T T G A A T A G T A A T T T G A A G A G	981	-
A T G T T T G T G T T T G A A T A G A G A A T A	982	-
T G A T A A A G A T A T G A G A G A T T G T A A	983	-
T A A A G A T G A G A T G T G T T A A A G T T	984	-
A A G T G A A A T T T G T A A G A A T T A G T G	985	-
G A A A T G A G A G T T A T T G A T A G T T T A	986	-
T T T G T A A A T G A G A T A T A G T G T T A G	987	-
G T T A A T T G T G A T A T T T G A T T A G T G	988	-
A G A G T G T T G A T A A A G A T G T T T A T A	989	-
A A T T G T G A G A A A T T G A T A A G A A G A	990	-
T T A A A G A G A A T T G A G A A G A G A A A T	991	-
T T G T T A G A A G A A T T G A A T G T A T G T	992	-
A G T T A A A G A T A T G T G T G A T G T T T A A	993	-
T G A G T T A T G T T G T A A T A G A A A T T G	994	-
T T A G A T A A G T T T A G A G A T T G A G A A	995	-
A T G A G T A A T A A G A G T A T T T G A A G T	996	-
T G T T T A A G T G T A A T G A T T T G T T A G	997	-
T T G A A G A A G A T T G T T A T T G T T G A A	998	-
T A T A G A A A G A T T A A A G A G T G A A T G	999	-
T A A A T T G T T A G A A A T T T G A G T G T G	1000	-
A T T G T T A G T G T G T T A T T G A T T A T G	1001	-
G A G A A T T A T G T G T G A A T A T A G A A A	1002	-
T T G A T T G A T A A A G T A A A G A G T G T A	1003	-
G T G T G T A A A A T T G A A T A T G T T A A T G	1004	-
A A A G A A A A G A A A G A A G T T T G A A A G	1005	-
T T T A G T T G A A G A A T A G A A A G A A A G	1006	-
G T G T A A T A A G A G T G A A T A G T A A T T	1007	-
T A T T G A A A T A A G A G A G A T T T G T G A	1008	-
A T G A G A A A G A A G A A G T T A A G A T T T	1009	-
A A G A G T G A G T A T A T T G T T A A A G A A	1010	-
T T T G T A A A G T G A T G A T G T A A G A T A	1011	-
G A T G T T A T G T G A T G A A A T A T G T A T	1012	-
T A G A A T A A A G T G T T A A A G T G T T A	1013	-
A A A G A G T A T G T G T G T A T G A T A T T T	1014	-
A A A G A T A A G A G T T A G T A A A T T G T G	1015	-
A A G A A T T A G A G A A T A A G T G T G A T A	1016	-
G A T A A G A A A G T G A A A T G T A A A T T G	1017	86
G A T G A A A G A T G T T T A A A G T T T G T T	1018	-
A G T G T A A G T A A T A A G T T T G A G A A A	1019	-
G T T G A G A A T T A G A A T T T G A T A A A G	1020	87
T T A A G A A A T T T G T A T G T T G T T G T T G	1021	-
A G A A G A T T T A G A T G A A A T G A G T T T	1022	-
T A A G T T T G A G A T A A A G A T G A T A T G	1023	-
T G A G A T A G T T T G T A A T A T G T T T G T	1024	-
A G T T T G A A A T T G T A A G T T T G A T G A	1025	-
T A G A A T T G A T T A A T G A T G A G T A G T	1026	-
A G A G A T T T G T A A T A A G T A T T G A A G	1027	-
A T A A T G A T G T A A T G T A A G T A G T G T	1028	-
T G A A A T T T G A T A G A G A G A T A T G T T A	1029	-
T G T G T A A A G T A T A G T T T A T G T T A G	1030	-
T G A A T A A G T G A A A T A G A A T G A A T G	1031	-



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Sequence	SEQ ID NO:	No. in Ex 1
AAAGAAAGATTGTAAATAAGTAGAG	1032	-
AATGAAATAGTGTAAATGAGTGT	1033	89
GTAGATAAAGATGTGAATTATGAT	1034	-
GATAGTATATGTGTGTATTTGTTT	1035	-
ATGTTTGTAGAAATGTTTGAAGAT	1036	-
AAATTTGTAGAGAGAAATTTGTTG	1037	-
TAGAAATAAGATTAGTAAGTGTAGA	1038	-
TGATTTTAGAGGAAATATGAGTAGAA	1039	-
AATAGAGTATGTGTATGAGGAA	1040	-
GATGATGAAGAGTTTATTTGTAAT	1041	-
AAGTAAAGAAAGAAAGAAATGTGTTA	1042	-
TTGAAGAATAATAAGTGTTTAGTGTAA	1043	-
AGAAAGAAATGTGTGATTTATGATGT	1044	-
GATTAAGAAGAGATGTGTGATTAAT	1045	-
AAATGATAATTGTGTGAGAGAGTAAT	1046	-
GTTTGTGTGAAAGTGTAAAGTATAAT	1047	90
TGAGTGTATATGAGAAAGTGTAAAT	1048	-
TTGTGAGAAAGAAAGTATATAGAAAT	1049	-
GTAAGTTTATAGAGTTATAGAGTTTA	1050	-
GATAGATAGATAAGTATAATTGAAG	1051	-
AGAGATGATTTGTTTATGTAATTATG	1052	-
AAAGTTAAGAAATAATTGTAGTGATAG	1053	-
TTTGTATATTGTTTGTGTGAGTGTATA	1054	-
ATTTGTAGAAAGTGTATGAGTTT	1055	-
GATTTGAGTAAAGTTTATAGATGAA	1056	-
AAGATAAAGTGAAGTTGATTTAGAT	1057	-
GATATTGTAAAGATATGTTGTAAAG	1058	-
GTAAGAGTGTATTTGTAAAGTTAATT	1059	-
GTGTGATTTAGTAAATGAAGTATTTA	1060	91
GTAAGAAAGATTAAAGTGTTAGTAA	1061	-
ATAGAGAAAGTTGAAATTGATTTATG	1062	92
TAAAGAGAAAGTTGAGTAAATGATTT	1063	-
GTTAAGAAATAAGTAGATAAAGTGAA	1064	-
TAAAGTAAATAATGAAAGTGTATAGTG	1065	-
AAGATGTATGTTTATTTGTGTGTATA	1066	-
ATTTAGAAATATAGTGAAGAGATAG	1067	-
GTTATGAAAGAGTATGTGTATAAAT	1068	93
TATTTATGTGAAGAGAAATGATTAG	1069	-
TAAATAAGTTGAAAGAAATGTTGT	1070	-
TGATGTTTGTATGTAATTGTTAAAG	1071	-
GTGAAAGATTTTGAGTTTGTATAAAT	1072	-
AGAGAAATATAGATTGAGATTTTGTT	1073	-
TTTGAAGATGTGATGATAAAGTTAA	1074	-
GTTGTATAAATTGTAGTAAAGAGTA	1075	94
GTGTTATGATGTGTGTTGTATTTAT	1076	-
ATTAATTGTGTAGATGTAATTAAAGAG	1077	-
GTTAGAAAGATTATGAGTTAGTT	1078	-
TTGTGTATTAAGAGAGGTGAAATAAT	1079	-
GTTTAAGATAGAAAGAGTGAATTTA	1080	-
AATGAGAAATAAGATAGTTATTGTG	1081	-
TGAATTGAAATAAGAAATTTGTTGTG	1082	95
AAATAAGATTGAAATTAGTGAAGTAAG	1083	-
AATGTTTGAAGAGATTTAGTAAGAA	1084	-
AGTTTAGAAATAGAAATGTTTGA	1085	-
TATAAGTAAGTGTTAAGATTTTGAG	1086	-
GTAGTGAAATAAGTGTAGTTAATA	1087	-
AAAGTGTGTATAAAGTAAATGTAGAT	1088	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
A G A G A T G T T T A T G T T G T G A A T T A A	1089	-
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T G A A T G T G A G A T G T T T A G A A T A A T	1091	-
A A T A A T G A T G T A A G T T T G A G T T T G	1092	-
A A A G A G T G A A T A G A A A T A A G A G A A	1093	-
A A T A A A G T T A T T G A G A G A G T T T A G	1094	-
A G T A G T G T T G T A G T T T A G T A T A T A	1095	-
G T A A G A A T G T A T T A G A T A T T T G T G	1096	-
G A T A A A T G T T T T G A T A A A G T A G T T G	1097	-
A T A G T A T G T A T G T G T G A A G A T T T A	1098	-
A T G A A T G T A G A G T G A T T A G T T T A A	1099	-
G T A G T A T T T A G T G A T G T A A G A A T A	1100	-
A G A A T T G T A T T G A A G A A G A A T A T G	1101	-
T T T A T A G A A T T G A G A G A A G T T A A G	1102	-
A A A G T A G T A G A G A T T T G A G A A T T A	1103	-
T T T A A A G A A A G T A T T G T A A G A G T G	1104	-
A A A T T G A G A A A G T G A A T G A A G T T T	1105	-
A A G A A A T A A G T A T G A T A G T A G T A G	1106	-
A T T T G A A T T G T A T T G T A G T T T G T G	1107	-
A A G A G A A T A A T G T A G A G A T A T A A G	1108	-
T G T G T A A T A G T T G T T A A T G A G T A A	1109	-
T A T A G T T G T A G T T T A G A T G A A T G T	1110	-
A T T G T G T T A G A A T G A T G T T A A T A G	1111	-
G T T T G T A T A G T A T T T G A T T G A T G T	1112	-
A G A G T A A A G T A T G A G T T A T G A A T A	1113	-
G A A A G T T T A A G T G A T G T A T A T T G T	1114	96
T T A A A T G A T A A A G A G T A G T G A A G T	1115	-
T T A A A T G T G T G A G A A G A T G A A T A A	1116	-
A T T T G T A T A A A G T G A A G A A G A G A A	1117	97
T G A T T A G T A T T T G T G A A G A G A T T T	1118	-
T T T G A A T G A A A T T G A T G A T A G A T G	1119	-
A G A G T A A G A T T A A G A A T A A G A A A G	1120	-
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G A A A G T T A G A G A A A T G T A G A A A T T	1124	-
G T G A A T A A T G A A G A A G T T A T G T T A	1125	98
T T G T G A A T A A A G T A G A T G T G T T A T	1126	-
T T A T A T G A T A T G A G T T T G T G T T G A	1127	-
T T G A T T T G T G T G A G T A T T A G T T A T	1128	-
A A A G T G A T T A A G T T A G T T T G A G A T	1129	-
T T G T A T T T G T A T A A T G T T G A A G A G	1130	-
G T T T G A A A T T A G T G T G A G A A A T A T	1131	-
A A T G T T G A G A T T G A T A A T G T T G A A	1132	-
T A G T A G T A G T A T T G T T G T A A T A A G	1133	-
G T T G T A A T T T G A G T G T T A G T T A T T	1134	-
T G A A T A T G A T A G T A G T A A T T G T G	1135	-
T G A T A G T A T G T T T G T G A T T A A A G A	1136	-
G A T G T A T A A A G A G T A T G T T A T A A G	1137	-
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A A A G A A T T A G T A T G A T A G A T G A G A	1140	99
T A G A G T T G T A T A G T T T A T A G T T G A	1141	-
G T A G A A T G A T T T G T T T A G A A G A T T T	1142	-
G T T T A T G T T T G A G A A G A G T T A T T T	1143	-
T A G A A G T T T G A A A G T T A T T G A T T G	1144	-
G A T G A A G A G T A T T T G T T A T A T G T A	1145	-

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Table I

Sequence	SEQ ID NO:	No. in Ex 1
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G A A A G A A A T T G A A G A G T T T G A T A T	1148	-
A T T T G A G T A T T T G T G T A T T G A A T G	1149	-
A T G A G T T G A A A T T T G A A G T A T T G T	1150	-
T T A A T A G T G A G A G A G T A T A T G T A A	1151	-
A T T A A G A G A G T G A G T A A A T G T A A A	1152	-
A A G A A T A G A T G A G A T T A G A A A T A G	1153	-
A G T T T A A A G A G T T A G A A T T G A A A G	1154	-
G T A A G A T T T G T T G A A T A A A G A A G A	1155	-
A G A G A A A G A A G T T A A A G T G A T A T T	1156	-
T A A T A G A G A A G A G A T G T A T G A A T A	1157	-
T T A T T A G T G A T A A G T G A A G T T T A G	1158	-
A T A A T G T A A A G A T G A G T T T A T G A G	1159	-
T T G A T T T G A G A G T T G A T A A G A T T T	1160	-
A T G A T T A A T T G T G T G T A G A A T T A G A	1161	-
T A T A A A G A T A T A G T A G A T G A T G T G	1162	-
T T T A G T T G A G A T G A A G T T A T T A G A	1163	-
A T T G A A T T G A T A T A G T G T A A A G T G	1164	-
G A A G A A A G A T T A T T G T A T T G A G T T	1165	-
A T T G A G T G T A G T G A T T T A G A A A T A	1166	-
A A T A A A G T G T T T A A G A G T A G A G T A	1167	-
G T A G A G A T A A T T G A T G T G T A A T T T	1168	-

All references referred to in this specification are incorporated herein by reference.

- 5 The scope of protection sought for the invention described herein is defined by the appended claims. It will also be understood that any elements recited above or in the claims, can be combined with the elements of any claim. In particular, elements of a dependent claim can be combined with any element of a claim from which it depends, or with
- 10 any other compatible element of the invention.

This application claims priority from United States Provisional Patent Application Nos. 60/263,710 and 60/303,799, filed January 25, 2001 and July 10, 2001. Both of these documents are incorporated herein by reference.

## CLAIMS

1. A composition comprising molecules for use as tags or tag  
complements wherein each molecule comprises an oligonucleotide selected  
5 from a set of oligonucleotides based on a following group of sequences,

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1 1 3 1 3 1 1 2 1 1 2 3 2 1 3 1 3 1 2 1 2 1 1 3  
2 3 2 3 2 1 1 2 1 3 2 2 3 2 2 1 1 2 3 1 3 2 1 1  
2 1 2 1 3 2 2 3 2 1 3 2 2 2 1 3 1 2 3 1 1 2 3 2  
1 2 2 3 2 3 2 2 1 3 1 1 2 3 1 2 3 2 2 1 1 2 1 3  
3 2 2 2 3 2 1 2 1 3 2 1 2 2 2 3 1 2 2 3 1 2 3 2  
1 3 1 3 2 1 1 1 3 2 1 2 3 1 3 2 2 1 2 3 1 1 2 1  
3 1 1 1 3 2 2 2 1 1 3 2 3 1 2 3 2 1 2 1 2 2 3 2  
2 2 1 1 1 2 3 1 2 1 1 1 3 1 3 2 1 3 2 3 1 1 3 2  
2 2 1 1 1 2 3 2 3 2 3 1 3 1 1 3 1 2 3 1 1 2 1 1  
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2 3 1 2 2 1 3 2 1 2 2 2 3 2 3 1 1 3 1 3 1 2 2 2  
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1 2 2 3 1 1 2 2 3 1 3 1 1 3 2 3 1 1 3 2 1 1 1 2  
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3 2 3 1 1 2 1 1 2 3 1 1 3 1 1 3 2 2 1 2 3 2 2 1  
2 2 3 2 3 1 1 2 1 1 1 3 2 1 3 1 2 3 2 3 2 2 1 2  
2 2 1 2 1 2 3 1 2 1 2 3 1 3 2 2 2 3 2 3 2 2 3 1  
2 2 3 1 2 2 2 3 2 3 2 3 1 3 2 1 2 2 1 3 2 2 1 2  
1 1 1 3 2 3 1 2 2 1 1 3 2 2 1 3 2 2 2 3 1 3 1 2  
2 2 3 2 1 2 2 2 3 2 1 2 1 1 2 3 2 2 3 1 1 3 1 3  
3 2 2 2 3 1 1 1 2 2 1 3 2 3 2 3 1 3 1 1 1 2 1 2  
1 1 2 3 2 2 3 1 3 1 2 2 3 1 2 1 1 2 3 2 2 3 1 1

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2 1 3 2 1 3 2 1 3 2 1 2 2 3 2 2 3 2 1 1 2 1 1 3
3 2 2 3 2 1 1 2 2 2 3 1 3 2 3 2 2 1 3 2 2 1 2 2
2 3 1 1 2 1 2 3 1 2 1 3 2 2 1 3 2 1 1 2 2 3 2 3
2 3 1 2 1 3 2 1 2 3 2 2 2 3 2 3 1 2 2 1 1 1 3 1
3 1 2 3 2 1 2 1 1 1 3 1 3 2 1 2 3 2 2 1 2 1 1 3
1 3 2 3 1 3 1 2 2 2 1 3 1 1 3 1 2 3 2 2 1 2 2 1
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2 1 1 2 1 3 1 3 1 1 3 1 3 1 2 3 2 1 2 3 1 1 2 1
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1 2 1 1 2 3 2 1 1 1 3 1 2 3 1 3 2 2 2 1 2 3 1 3
2 2 3 1 2 2 2 3 1 3 1 3 2 2 3 1 2 1 1 3 1 2 2 2
1 2 3 1 2 2 1 2 2 3 2 3 2 3 2 1 3 1 1 2 2 1 3 1
2 1 2 1 1 1 3 1 2 1 2 1 3 2 1 3 1 2 3 1 2 3 2 3
2 2 2 1 3 2 2 3 1 3 1 2 3 1 1 3 2 2 1 2 2 1 3 1
1 2 2 3 1 1 2 2 3 1 2 1 2 1 3 2 3 2 1 1 1 3 2 3
3 1 1 3 1 1 1 3 1 2 2 1 2 2 3 2 1 2 2 3 1 3 2 2
1 2 2 3 1 3 2 3 2 1 3 2 3 1 2 2 2 1 3 1 1 1 2 1
1 1 2 1 1 1 3 2 3 2 2 2 1 1 3 1 3 2 1 3 1 3 2 1
3 2 1 3 1 3 1 2 1 1 2 2 3 1 2 3 2 3 2 1 1 2 2 2

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wherein each of 1 to 3 is a nucleotide base selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base

5 provided that:

for any pair of sequences of the set:

$M1 \leq 15$ ,  $M2 \leq 12$ ,  $M3 \leq 19$ ,  $M4 \leq 15$ , and  $M5 \leq 18$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches

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having a length of at least 3, for any alignment of maximum score;  
wherein:

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):

- (i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,
- (ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,
- (iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and
- (iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;  
B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

2. A composition comprising molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on a group of sequences having the numeric pattern of sequences set out in claim 1, wherein each of 1 to 3 is a nucleotide base selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base provided that:

for any pair of sequences of the set:

$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of maximum score;

wherein

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):



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- (i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,
- (ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,
- (iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and
- (iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;  
 B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

3. A composition comprising molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide selected from a set of oligonucleotides based on a group of sequences having the numeric patterns set out in claim 1, wherein each of 1 to 3 is a nucleotide base selected to be different from the others of 1 to 3 with the proviso that up to three nucleotide bases of each sequence can be substituted with any nucleotide base provided that:

for any pair of sequences of the set:

$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment;

M3 is the maximum number of matches for any alignment having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of maximum score, wherein:

the score of an alignment is determined according to the equation  $3A$

$- B - 3C - D$ , wherein:

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

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4. A composition according to any preceding claim, wherein for the group of 24mer sequences in which 1 = A, 2 = T and 3 = G, under a defined set of conditions in which the maximum degree of hybridization  
5 between a sequence and any complement of a different sequence of the group of 24mer sequences does not exceed 30% of the degree of hybridization between said sequence and its complement, for all said oligonucleotides of the composition, the maximum degree of hybridization between an oligonucleotide and a complement of any other oligonucleotide  
10 of the composition does not exceed 50% of the degree of hybridization of the oligonucleotide and its complement.

5. The composition of claim 4, wherein said maximum degree of hybridization between a sequence and any complement of a different  
15 sequence does not exceed 30% of the degree of hybridization between said sequence and its complement, the degree of hybridization between each sequence and its complement varies by a factor of between 1 and up to 10, more preferably between 1 and up to 9, more preferably between 1 and up to 8, more preferably between 1 and up to 7, more preferably between  
20 1 and up to 6, and more preferably between 1 and up to 5.

6. The composition of claim 4 or 5, wherein the maximum degree of hybridization between a sequence and any complement of a different sequence does not exceed 25%, more preferably does not exceed 20%, more  
25 preferably does not exceed 15%, more preferably does not exceed 10%, more preferably does not exceed 5%.

7. The composition of any of claims 4 to 6, wherein said defined set of conditions results in a level of hybridization that is the same as the  
30 level of hybridization obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C.

8. The composition of any of claims 4 to 7, said defined set of conditions includes the group of 24mer sequences being covalently linked  
35 to beads.

9. The composition of claim 4 wherein, for the group of 24mers the maximum degree of hybridization between a sequence and any complement of a different sequence does not exceed 15% of the degree of hybridization  
40 between said sequence and its complement and the degree of hybridization

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between each sequence and its complement varies by a factor of between 1 and up to 9, and for all oligonucleotides of the set, the maximum degree of hybridization between an oligonucleotide and a complement of any other oligonucleotide of the set does not exceed 20% of the degree of hybridization of the oligonucleotide and its complement.

10. The composition of any preceding claim wherein: each 1 is one of A, T/U, G and C; each 2 is one of A, T/U, G and C; and each 3 is one of A, T/U, G and C; and each of 1, 2 and 3 is selected so as to be different from all of the others of 1, 2 and 3.

11. The composition of claim 10, wherein 1 is A or T/U, 2 is A or T/U and 3 is G or C.

12. The composition of claim 11, wherein 1 is A, 2 is T/U and 3 is G.

13. The composition of any preceding claim, wherein each said oligonucleotide is from twenty-two to twenty-six bases in length, or from twenty-three to twenty-five.

14. The composition of any of claims 1 to 13, wherein each said oligonucleotide is of the same length as every other said oligonucleotide.

15. The composition of claim 14, wherein each said oligonucleotide is twenty-four bases in length.

16. The composition of any of claims 1 to 13 wherein no said oligonucleotide contains more than four contiguous bases that are identical to each other.

17. The composition of any of claims 1 to 12 and 16 wherein the number of G's in each said oligonucleotide does not exceed  $L/4$  where L is the number of bases in said sequence.

18. The composition of any of claims 1 to 14 and 16 and 17, wherein the number of G's in each said oligonucleotide does not vary from the average number of G's in all of the said oligonucleotides by more than one.

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19. The composition of any claims 1 to 14 and 16 to 18, wherein the number of G's in each said oligonucleotide is the same as every other said oligonucleotide.

5 20. The composition of claim 19, wherein each said oligonucleotide is twenty-four bases in length and each said oligonucleotide contains 6 G's.

10 21. The composition of any of claims 1 to 12 and claims 16 to 20, wherein, for each said nucleotide, there is at most six bases other than G between every pair of neighboring pairs of G's.

15 22. The composition of any of claims 1 to 12 and claims 16 to 21, wherein at the 5'-end of each said oligonucleotide at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence of the oligonucleotide is a G.

20 23. The composition of any of claims 1 to 12 and claims 16 to 21, wherein at the 3'-end of each said oligonucleotide at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence of the oligonucleotide is a G.

25 24. The composition of claim 22, wherein at the 3'-end of each said oligonucleotide at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence of the oligonucleotide is a G.

30 25. The composition of any of claims 1 to 24, comprising ten, or twenty, or thirty, or forty, or fifty, or sixty, or seventy, or eighty, or ninety, or one hundred, or one hundred and ten, or one hundred and twenty, or one hundred and thirty, or one hundred and forty, or one hundred and fifty, or one hundred and sixty said molecules, or comprising one hundred and seventy said molecules, or comprising one hundred and eighty said molecules, or comprising one hundred and ninety said molecules, or comprising two hundred said molecules, or comprising two hundred and twenty said molecules, or comprising two hundred and forty  
35 said molecules, or comprising two hundred and sixty said molecules, or comprising two hundred and eighty said molecules, or comprising three hundred said molecules, or comprising four hundred said molecules, or comprising five hundred said molecules, or comprising six hundred said  
40 molecules, or comprising seven hundred said molecules, or comprising

eight hundred said molecules, or comprising nine hundred said molecules, or comprising one thousand said molecules, eleven hundred said molecules.

5 26. A composition of any of claims 1 to 25, wherein each said molecule is linked to a solid phase support so as to be distinguishable from a mixture of other said molecules by hybridization to its complement.

10 27. The composition of claim 26, wherein each molecule is linked to a defined location on a said solid phase support, the defined location for each said molecule being different than the defined location for different other said molecules.

15 28. The composition of claim 27, wherein each said solid phase support is a microparticle and each said molecule is covalently linked to a different microparticle than each other different said molecule.

20 29. A composition comprising a set of 150 molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide having a sequence of at least sixteen nucleotide bases wherein for any pair of sequences of the set:

$M1 > 19/24 \times L1$ ,  $M2 > 17/24 \times L1$ ,  $M3 > 21/24 \times L1$ ,  $M4 > 18/24 \times L1$ ,  $M5 > 20/24 \times L1$ , where  $L1$  is the length of the shortest sequence of the pair, where:

$M1$  is the maximum number of matches for any alignment of the pair of sequences in which there are no internal indels;

$M2$  is the maximum length of a block of matches for any alignment of the pair of sequences;

$M3$  is the maximum number of matches for any alignment of the pair of sequences having a maximum score;

$M4$  is the maximum sum of the lengths of the longest two blocks of matches for any alignment of the pair of sequences of maximum score; and

$M5$  is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of the pair of sequences of maximum score, wherein:

the score of an alignment is determined according to the equation  $(A \times m) - (B \times mm) - (C \times (og + eg)) - (D \times eg)$ , wherein:

for each of (i) to (iv):

(i)  $m = 6$ ,  $mm = 6$ ,  $og = 0$  and  $eg = 6$ ,

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- (ii)  $m = 6$ ,  $mm = 6$ ,  $og = 5$  and  $eg = 1$ ,
- (iii)  $m = 6$ ,  $mm = 2$ ,  $og = 5$  and  $eg = 1$ , and
- (iv)  $m = 6$ ,  $mm = 6$ ,  $og = 6$  and  $eg = 0$ ,

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment; and

wherein the maximum score is determined separately for each of (i), (ii), (iii) and (iv).

30. A composition comprising a set of 150 molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide having a sequence of at least sixteen nucleotide bases wherein for any

5 pair of sequences of the set:

$M1 \leq 18$ ,  $M2 \leq 16$ ,  $M3 \leq 20$ ,  $M4 \leq 17$ , and  $M5 \leq 19$ , where:

M1 is the maximum number of matches for any alignment of the pair of sequences in which there are no internal indels;

M2 is the maximum length of a block of matches for any alignment of the pair of sequences;

M3 is the maximum number of matches for any alignment of the pair of sequences having a maximum score;

M4 is the maximum sum of the lengths of the longest two blocks of matches for any alignment of the pair of sequences of maximum score; and

M5 is the maximum sum of the lengths of all the blocks of matches having a length of at least 3, for any alignment of the pair of sequences of maximum score, wherein:

the score of a said alignment is determined according to the equation

$3A - B - 3C - D$ , wherein:

A is the total number of matched pairs of bases in the alignment;

B is the total number of internal mismatched pairs in the alignment;

C is the total number of internal gaps in the alignment; and

D is the total number of internal indels in the alignment minus the total number of internal gaps in the alignment.

31. The composition of claim 29 or 30, wherein each said sequence has up to fifty bases.

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32. The composition of claim 31, wherein each said sequence is between sixteen and forty bases in length, or between sixteen and thirty-five bases in length, or between eighteen and thirty bases in length, or  
5 between twenty and twenty-eight bases in length, or between twenty-one and twenty-seven bases in length, or between twenty-two and twenty-six bases in length.

10 33. The composition of any of claims 29 to 32, wherein each said sequence is of the same length as every other said sequence.

34. The composition of claim 33, wherein each said sequence is twenty-four bases in length.

15 35. The composition of any of claims 29 to 34 wherein no said sequence contains more than four contiguous bases that are identical to each other.

20 36. The composition of any of claims 29 to 35 wherein the number of G's in each said sequence does not exceed  $L/4$  where L is the number of bases in said sequence.

25 37. The composition of claim 36, wherein the number of G's in each said sequence does not vary from the average number of G's in all of the sequences of the set by more than one.

38. The composition of claim 37, wherein the number of G's in each said sequence is the same as every other sequence of the set.

30 39. The composition of claim 37, wherein each said sequence is twenty-four bases in length and each said sequence contains 6 G's.

35 40. The composition of any of claims 29 to 39 wherein, for each said sequence, there is at most six bases other than G between every pair of neighboring pairs of G's.

41. The composition of any of claims 29 to 40, wherein at the 5'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

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42. The composition of any of claims 29 to 40, wherein at the 3'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

5 43. The composition of claim 41, wherein at the 3'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

10 44. The composition of any of claims 29 to 43, wherein under a defined set of conditions, the maximum degree of hybridization between a said oligonucleotide and any complement of a different oligonucleotide of the composition does not exceed about 30% of the degree of hybridization between said oligonucleotide and its complement, more preferably 20%, more preferably 15%, more preferably 10%, more preferably 6%.

15 45. The composition of claim 44, wherein said set of conditions results in a level of hybridization that is the same as the level of hybridization obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C, and the oligonucleotides  
20 are covalently linked to microparticles.

46. The composition of claim 45, wherein under said defined set of conditions, the degree of hybridization between each oligonucleotide and its complement varies by a factor of between 1 and up to 8, more  
25 preferably up to 7, more preferably up to 6, more preferably up to 5.

47. The composition of any of claims 29 to 46, comprising one hundred and sixty said molecules, or comprising one hundred and seventy said molecules, or comprising one hundred and eighty said molecules, or  
30 comprising one hundred and ninety said molecules, or comprising two hundred said molecules, or comprising two hundred and twenty said molecules, or comprising two hundred and forty said molecules, or comprising two hundred and sixty said molecules, or comprising two hundred and eighty said molecules, or comprising three hundred said  
35 molecules, or comprising four hundred said molecules, or comprising five hundred said molecules, or comprising six hundred said molecules, or comprising seven hundred said molecules, or comprising eight hundred said molecules, or comprising nine hundred said molecules, or comprising one thousand said molecules.

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48. A composition of any of claims 29 to 47, wherein each said molecule is linked to a solid phase support so as to be distinguishable from a mixture of other said molecules by hybridization to its complement.

5 49. The composition of claim 48, wherein each molecule is linked to a defined location on a said solid phase support, the defined location for each said molecule being different than the defined location for different other said molecules.

10 50. The composition of claim 49, wherein each said solid phase support is a microparticle and each said molecule is covalently to a different microparticle than each other different said molecule.

15 51. A composition comprising one hundred and fifty minimally cross-hybridizing molecules for use as tags or tag complements wherein each molecule comprises an oligonucleotide comprising a sequence of nucleotide bases for which, under a defined set of conditions, the maximum degree of hybridization between a said oligonucleotide and any complement of a different oligonucleotide does not exceed about 20% of  
20 the degree of hybridization between said oligonucleotide and its complement.

52. The composition of claim 51, wherein each said sequence has between ten and fifty bases.

25

53. The composition of claim 52, wherein each said sequence is between sixteen and forty bases in length, or between sixteen and thirty-five bases in length, or between eighteen and thirty bases in length, or between twenty and twenty-eight bases in length, or between twenty-one  
30 and twenty-seven bases in length, or between twenty-two and twenty-six bases in length.

54. The composition of any of claims 51 to 53, wherein each said sequence is of the same length as every other said sequence.

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55. The composition of claim 54, wherein each said sequence is twenty-four bases in length.

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56. The composition of any of claims 51 to 55 wherein no said sequence contains more than four contiguous bases that are identical to each other.

5 57. The composition of any of claims 51 to 56 wherein the number of G's in each said sequence does not exceed  $L/4$  where L is the number of bases in said sequence.

10 58. The composition of claim 57, wherein the number of G's in each said sequence does not vary from the average number of G's in all of the sequences of the set by more than one.

59. The composition of claim 58, wherein the number of G's in each said sequence is the same as every other sequence of the set.

15

60. The composition of claim 58, wherein each said sequence is twenty-four bases in length and each said sequence contains 6 G's.

20 61. The composition of any of claims 51 to 60 wherein, for each said sequence, there is at most six bases other than G between every pair of neighboring pairs of G's.

25 62. The composition of any of claims 51 to 61, wherein at the 5'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

30 63. The composition of any of claims 51 to 61, wherein at the 3'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

64. The composition of claim 62, wherein at the 3'-end of each said sequence at least one of the first, second, third, fourth, fifth, sixth and seventh bases of the sequence is a G.

35 65. The composition of any of claims 61 to 64, wherein under a said defined set of conditions, the maximum degree of hybridization between a said oligonucleotide and any complement of a different oligonucleotide of the composition does not exceed about 15%, more preferably 10%, more preferably 6%.

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66. The composition of claim 65, wherein said set of conditions results in a level of hybridization that is the same as the level of hybridization obtained when hybridization conditions include 0.2 M NaCl, 0.1 M Tris, 0.08% Triton X-100, pH 8.0 at 37°C, and the oligonucleotides are covalently linked to microparticles.

67. The composition of claim 66, wherein under said defined set of conditions, the degree of hybridization between each oligonucleotide and its complement varies by a factor of between 1 and up to 8, more preferably up to 7, more preferably up to 6, more preferably up to 5.

68. The composition of any of claims 51 to 67, comprising one hundred and sixty said molecules, or comprising one hundred and seventy said molecules, or comprising one hundred and eighty said molecules, or comprising one hundred and ninety said molecules, or comprising two hundred said molecules, or comprising two hundred and twenty said molecules, or comprising two hundred and forty said molecules, or comprising two hundred and sixty said molecules, or comprising two hundred and eighty said molecules, or comprising three hundred said molecules, or comprising four hundred said molecules, or comprising five hundred said molecules, or comprising six hundred said molecules, or comprising seven hundred said molecules, or comprising eight hundred said molecules, or comprising nine hundred said molecules, or comprising one thousand said molecules.

69. A composition of any of claims 51 to 68, wherein each said molecule is linked to a solid phase support so as to be distinguishable from a mixture of other said molecules by hybridization to its complement.

70. The composition of claim 69, wherein each molecule is linked to a defined location on a said solid phase support, the defined location for each said molecule being different than the defined location for different other said molecules.

71. The composition of claim 70, wherein each said solid phase support is a microparticle and each said molecule is covalently to a different microparticle than each other different said molecule.

72. A composition according to any of claims 1 to 71, wherein each said molecule comprises a tag complement.

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73. A composition according to any of claims 1 to 72, wherein any base is substituted by an analogue thereof.

74. A composition according to any of claims 1 to 73, wherein each said molecule comprises a tag complement.

75. A kit for sorting and identifying polynucleotides, the kit comprising one or more solid phase supports each having one or more spatially discrete regions, each such region having a uniform population of substantially identical tag complements covalently attached, and the tag complements each being selected from the set of oligonucleotides as defined in any of claims 1 to 84.

76. A kit according to claim 75, wherein there is a tag complement for each said oligonucleotide of a said composition.

77. A kit according to claim 75 or 76 wherein said one or more solid phase supports is a planar substrate and wherein said one or more spatially discrete regions is a plurality of spatially addressable regions.

78. A kit according to any of claims 75 to 77 wherein said one or more solid phase supports is a plurality of microparticles.

79. A kit according to claim 78 wherein said microparticles each have a diameter in the range of from 5 to 40  $\mu\text{m}$ .

80. A kit according to claim 78 or 79, wherein each microparticle is spectrophotometrically unique from each other microparticle having a different oligonucleotide attached thereto.

81. A method of analyzing a biological sample comprising a biological sequence for the presence of a mutation or polymorphism at a locus of the nucleic acid, the method comprising:

- (A) amplifying the nucleic acid molecule in the presence of a first primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements as defined in claim 74 to form an amplified molecule with a 5'-end with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecule in the presence of a polymerase and a

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- second primer having 5'-end complementary the 3'-end of the amplified sequence, with the 3'-end of the second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is: (i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus of the amplified sequence;
- (C) specifically hybridizing the second primer to a tag complement having the tag complement sequence of (A); and
  - (D) detecting the nucleotide derivative incorporated into the second primer in (B) so as to identify the base located at the locus of the nucleic acid.

82. A method of analyzing a biological sample comprising a plurality of nucleic acid molecules for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for each nucleic acid molecule,

5 the method comprising:

- (A) amplifying the nucleic acid molecule in the presence of a first primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements as defined in claim 74 to form an amplified molecule with a 5'-end with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecule in the presence of a polymerase and a second primer having 5'-end complementary the 3'-end of the amplified sequence, the 3'-end of the second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is: (i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus of the amplified molecule;
- (C) specifically hybridizing the second primer to a tag complement having the tag complement sequence of (A); and
- (D) detecting the nucleotide derivative incorporated into the second primer in (B) so as to identify the base located at the locus of the nucleic acid;

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wherein each tag of (A) is unique for each nucleic acid molecule and steps (A) and (B) are carried out with said nucleic molecules in the presence of each other.

83. A method of analyzing a biological sample comprising a plurality of double stranded complementary nucleic acid molecules for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for  
5 each nucleic acid molecule, the method comprising:

- (A) amplifying the double stranded molecule in the presence of a pair of first primers, each primer having an identical 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements as defined in claim 74 to form amplified molecules with 5'-ends with a sequence complementary to the sequence of the tag;
- (B) extending the amplified molecules in the presence of a polymerase and a pair of second primers each second primer having a 5'-end complementary a 3'-end of the amplified sequence, the 3'-end of each said second primer extending to immediately adjacent said locus, in the presence of a plurality of nucleoside triphosphate derivatives each of which is:
  - (i) capable of incorporation during transcription by the polymerase onto the 3'-end of a growing nucleotide strand; (ii) causes termination of polymerization; and (iii) capable of differential detection, one from the other;
- (C) specifically hybridizing each of the second primers to a tag complement having the tag complement sequence of (A); and
- (D) detecting the nucleotide derivative incorporated into the second primers in (B) so as to identify the base located at said locus;

wherein the sequence of each tag of (A) is unique for each nucleic acid molecule and steps (A) and (B) are carried out with said nucleic molecules in the presence of each other.

84. A method of analyzing a biological sample comprising a plurality of nucleic acid molecules for the presence of a mutation or polymorphism at a locus of each nucleic acid molecule, for each nucleic acid molecule,  
10 the method comprising:

- (a) hybridizing the molecule and a primer, the primer having a 5'-sequence having the sequence of a tag complementary to the sequence of a tag complement belonging to a family of tag complements as defined in claim 74 and a 3'-end extending to immediately adjacent the locus;
- (b) enzymatically extending the 3'-end of the primer in the presence of a

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plurality of nucleoside triphosphate derivatives each of which is: (i) capable of enzymatic incorporation onto the 3'-end of a growing nucleotide strand; (ii) causes termination of said extension; and (iii) capable of differential detection, one from the other, wherein there is a said derivative complementary to each possible nucleotide present at said locus;

- (c) specifically hybridizing the extended primer formed in step (b) to a tag complement having the tag complement sequence of (a); and
- (d) detecting the nucleotide derivative incorporated into the primer in step (b) so as to identify the base located at the locus of the nucleic acid molecule;

wherein each tag of (a) is unique for each nucleic acid molecule and steps (a) and (b) are carried out with said nucleic molecules in the presence of each other.

85. The method of claim 82 wherein each said derivative is a dideoxy nucleoside triphosphate.

- 5 86. The method of claim 84, wherein each respective complement is attached as a uniform population of substantially identical complements in a spatially discrete region on one or more said solid phase supports.

- 10 87. The method of claim 86, each said tag complement comprises a label, each such label being different for respective complements, and step (d) includes detecting the presence of the different labels for respective hybridization complexes of bound tags and tag complements.

- 15 88. The hybridized molecule and primer of step (A) of any of claims 84 to 87.

89. A method of determining the presence of a target suspected of being contained in a mixture, the method comprising the steps of:

- (i) labelling the target with a first label;
- (ii) providing a first detection moiety capable of specific binding to the target and including a first tag;
- (iii) exposing a sample of the mixture to the detection moiety under conditions suitable to permit (or cause) said specific binding of the molecule and target;
- (iv) providing a family of tag complements as defined in claim 74 wherein the family contains a first tag complement having a sequence

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complementary to that of the first tag;

- (v) exposing the sample to the family of tag complements under conditions suitable to permit (or cause) specific hybridization of the first tag and its tag complement;
- (vi) determining whether a said first detection moiety hybridized to a first said tag complement is bound to a said labelled target in order to determine the presence or absence said target in the mixture.

90. The method of claim 89 wherein said first tag complement is linked to a solid support at a specific location of the support and step (vi) includes detecting the presence the first label at said specified  
5 location.

91. The method of claim 89 wherein said first tag complement comprises a second label and step (vi) includes detecting the presence of the first and second labels in a hybridized complex of the moiety and the  
10 first tag complement.

92. The method of claim 89 wherein said target is selected from the group consisting of organic molecules, antigens, proteins, polypeptides, antibodies and nucleic acids.  
15

93. The method of claim 92, wherein said target is an antigen and said first molecule is an antibody specific for said antigen.

94. The method of claim 93, wherein the antigen is a polypeptide or  
20 protein and the labelling step includes conjugation of fluorescent molecules, digoxigenin, biotinylation and the like.

95. The method of claim 94, wherein said target is a nucleic acid and the labelling step includes incorporation of fluorescent molecules,  
25 radiolabelled nucleotide, digoxigenin, biotinylation and the like.



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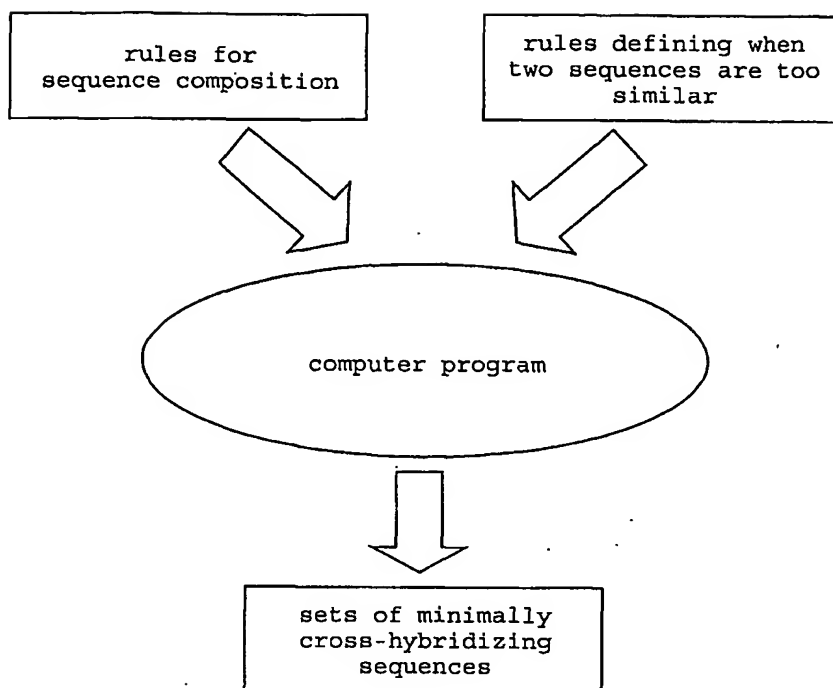
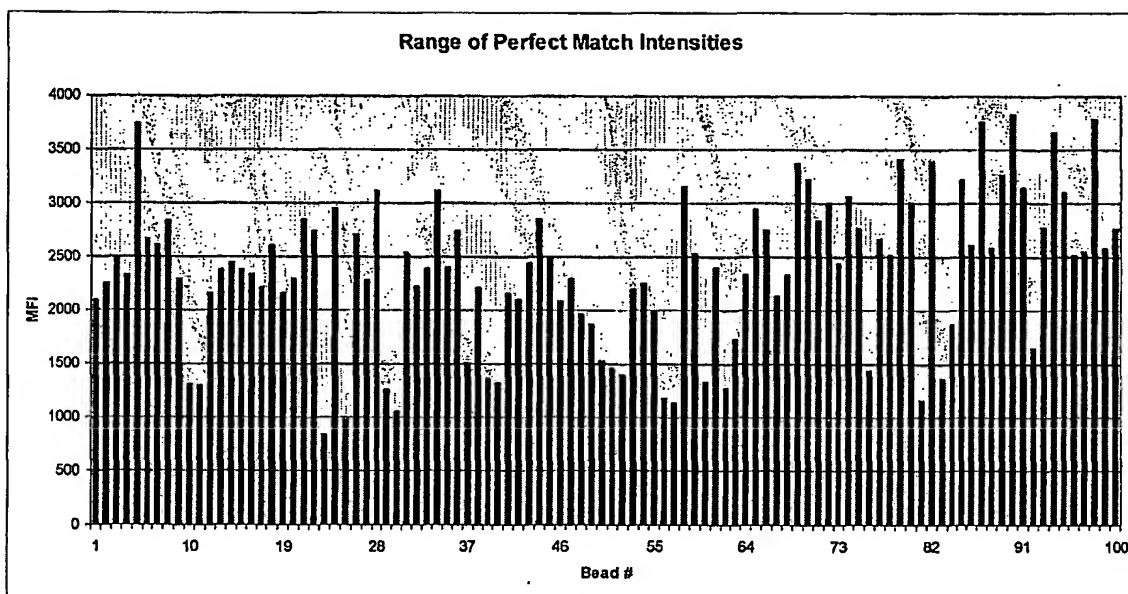


Figure 1

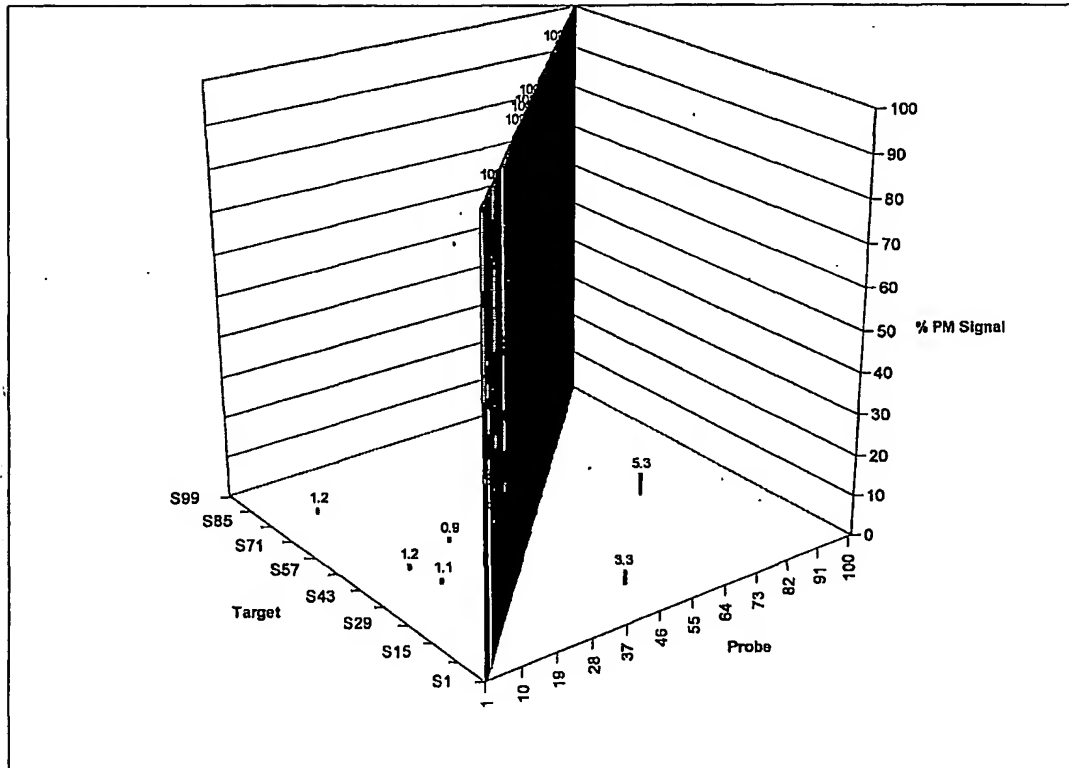
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Figure 2



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Figure 3



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Figure 4

Bead/Probe 90

